```
;       NAME:  Svoboda, Craig G.
;       REGISTRATION NUMBER:  39,044
;       REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650/225-1489
;       TELEFAX:  650/952-9881
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  453 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-08-466-151-8

  Query Match             46.6%;  Score 1259;  DB 3;  Length 453;
  Best Local Similarity   58.9%;  Pred. No. 9.1e-90;
  Matches  271;  Conservative   26;  Mismatches   87;  Indels   76;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL 86
              | : | :: |:|  |          ::|      | |     |    | :   |    | ::
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYADSVKGRFTI 70

Qy         87 W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL---QGQSLT 140
                 :  | | : :|: ||:  | |              ||       |     ||  :|
Db         71 SRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-------YFG-----HWHFAVWGQGTLVT 118

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              ::  |  |  |||   :|  |:  ||             : ::||
Db        119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
              || ||                |: | |  | |    |:|       ||||||||||
Db        179 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 232

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 292

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 352

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              |||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 412

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        413 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 452


RESULT 57
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Immunoglobulin Variants
;  FILE REFERENCE: P0718P2C1D1
;  CURRENT APPLICATION NUMBER: US/08/466,163B
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-08-466-163B-8

  Query Match             46.6%;  Score 1259;  DB 4;  Length 453;
  Best Local Similarity   58.9%;  Pred. No. 9.1e-90;
  Matches  271;  Conservative   26;  Mismatches   87;  Indels   76;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL 86
              | : | :: |:|  |          ::|      | |     |    | :   |    | ::
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYADSVKGRFTI 70

Qy         87 W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL---QGQSLT 140
                 :  | | : :|: ||:  | |              ||       |     ||  :|
Db         71 SRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-------YFG-----HWHFAVWGQGTLVT 118

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              ::  |  |  |||   :|  |:  ||             : ::||
Db        119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
              || ||                |: | |  | |    |:|       ||||||||||
Db        179 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 232

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 292

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 352

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              |||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 412

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        413 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 452


RESULT 58
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION:  Method of Preventing the Onset of Allergic Disorders (as amende
;  FILE REFERENCE:  P0718P2C3US
;  CURRENT APPLICATION NUMBER: US/09/802,096
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  US 08/405,617
;  PRIOR FILING DATE:  1995-03-15
;  PRIOR APPLICATION NUMBER:  US 08/185,899
;  PRIOR FILING DATE:  1994-01-26
;  PRIOR APPLICATION NUMBER:  PCT/US92/06860
;  PRIOR FILING DATE:  1992-08-14
;  PRIOR APPLICATION NUMBER:  US 07/879,495
;  PRIOR FILING DATE:  1992-05-07
;  PRIOR APPLICATION NUMBER:  US 07/744,768
;  PRIOR FILING DATE:  1991-08-14
;  NUMBER OF SEQ ID NOS:  64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-096-8

  Query Match             46.6%;  Score 1259;  DB 4;  Length 453;
```

```
  Best Local Similarity   58.9%;  Pred. No. 9.1e-90;
  Matches  271;  Conservative   26;  Mismatches   87;  Indels   76;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL 86
              | : | :: |:|  |          ::|     | |     |     | :   |    | ::
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYADSVKGRFTI 70

Qy         87 W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL---QGQSLT 140
                :  | | : :|: ||:  | |           ||        |     ||  :|
Db         71 SRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-------YFG-----HWHFAVWGQGTLVT 118

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              ::  |  |  |||   :|  |:  ||             : ::||
Db        119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                 |: | |  | |    |:|       ||||||||||
Db        179 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 232

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 292

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 352

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              |||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||
Db        353 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 412

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        413 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 452


RESULT 59
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-10

  Query Match           46.6%;  Score 1259;  DB 2;  Length 476;
  Best Local Similarity   66.2%;  Pred. No. 9.8e-90;
  Matches  258;  Conservative   17;  Mismatches   45;  Indels   70;  Gaps    8;

Qy         96 IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL-----QGQSLTLTLESPPGSS 150
              : :|: ||:  | |  :  ::          || |   :      ||   :|: |
Db        102 LTSLRSEDTAVYYCATDRYRQ----------ANFDRARVGWFDPWGQGTLVTVSSASTKG 151

Qy        151 PSVQCRSPRGKNIQGG------------KTLSVS------------QLELQDSG---- 180
              |||   :|  |:  ||             : ::||            || ||
Db        152 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 211

Qy        181 -------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLG 221
                          |: | |  | |    |:|       ||||||||||     |||||
Db        212 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 265

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 325

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 385

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 445

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||
Db        446 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 60
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,550
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
```

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;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 478 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-487-550-8

  Query Match             46.6%;  Score 1259;  DB 3;  Length 478;
  Best Local Similarity   66.9%;  Pred. No. 9.8e-90;
  Matches  259;  Conservative   12;  Mismatches   56;  Indels   60;  Gaps    7;

Qy         94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV 153
              | : :|||||:  | |           |          ||   :|: |     |||
Db        102 LQMSSLKIEDTAVYYCTTSYISH-----CRGGVCYGGYFEFWGQGALVTVSSASTKGPSV 156

Qy        154 QCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG------- 180
                :|  |:  ||              : ::||              || ||
Db        157 FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV 216

Qy        181 -----------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPS 224
                        |: | |  | |    |:|       ||||||||||     ||||||||
Db        217 VTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPS 270

Qy        225 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 330

Qy        285 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 390

Qy        345 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 450

Qy        405 GNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||
Db        451 GNVFSCSVMHEALHNHYTQKSLSLSPG 477


RESULT 61
US-09-526-098-8
; Sequence 8, Application US/09526098
; Patent No. 6492134
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/526,098
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/383,916
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/487,550
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 478 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-526-098-8

  Query Match             46.6%;  Score 1259;  DB 4;  Length 478;
  Best Local Similarity   66.9%;  Pred. No. 9.8e-90;
  Matches  259;  Conservative   12;  Mismatches   56;  Indels   60;  Gaps    7;

Qy         94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV 153
              | : :|||||:  | |           |          ||   :|: |     |||
Db        102 LQMSSLKIEDTAVYYCTTSYISH-----CRGGVCYGGYFEFWGQGALVTVSSASTKGPSV 156

Qy        154 QCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG------- 180
                :|  |:  ||              : ::||              || ||
Db        157 FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV 216

Qy        181 -----------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPS 224
                        |: | |  | |    |:|       ||||||||||     ||||||||
Db        217 VTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPS 270

Qy        225 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 330

Qy        285 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 390

Qy        345 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 450

Qy        405 GNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||
Db        451 GNVFSCSVMHEALHNHYTQKSLSLSPG 477


RESULT 62
US-09-499-846-10
; Sequence 10, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh et al.
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: 035784/195012 (5784-
;  CURRENT APPLICATION NUMBER: US/09/499,846
;  CURRENT FILING DATE:  2000-02-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-499-846-10

  Query Match             46.6%;  Score 1258.5;  DB 4;  Length 497;
  Best Local Similarity   57.1%;  Pred. No. 1.1e-89;
  Matches  274;  Conservative   30;  Mismatches   85;  Indels   91;  Gaps   12;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
              :|  :|||             ||:  | :|   :    | ||  : |    | | :  :
```

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Db         45 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 92

Qy         70 TKG-------PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |          ||              |:||:  |::|     : ||  :| ::     :|
Db         93 TWSIIMDSVVPS------------DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 139

Qy        123 FGLTANSDTHLLQGQSLTLTLESPP-------------GSS------PSVQCRSPRGKNI 163
              || ||    |          : | |              ||       | ||     | |
Db        140 AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT 199

Qy        164 --QGGKTLSVSQLELQDSGTWTC--------------TVLQNQKKVEFKIDIVPCP--- 203
                :  : | :  :  :|:| :||              |||:    :| :  ::  |
Db        200 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 256

Qy        204 -------APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                    ||||||||||||     ||| ||||||||||||||||||||||||||||||||
Db        257 EGSGSPGLQEPKSCDKTHTCPPCPAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 316

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 376

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 436

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 496
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RESULT 63
US-09-499-846-8
; Sequence 8, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-8

Query Match 46.6%; Score 1258.5; DB 4; Length 525;
Best Local Similarity 57.1%; Pred. No. 1.2e-89;
Matches 274; Conservative 30; Mismatches 85; Indels 91; Gaps 12;

```
Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
              :|  :|||              ||:  | :|   :    | ||  : |    | | :  :
Db         73 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120

Qy         70 TKG-------PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |          ||              |:||:  |::|     : ||  :| ::     :|
Db        121 TWSIIMDSVVPS------------DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 167

Qy        123 FGLTANSDTHLLQGQSLTLTLESPP-------------GSS------PSVQCRSPRGKNI 163
              || ||    |          : | |              ||       | ||     | |
Db        168 AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT 227

Qy        164 --QGGKTLSVSQLELQDSGTWTC--------------TVLQNQKKVEFKIDIVPCP--- 203
                :  : | :  :  :|:| :||              |||:    :| :  ::  |
Db        228 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 284

Qy        204 -------APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                    ||||||||||||     ||| ||||||||||||||||||||||||||||||||
Db        285 EGSGSPGLQEPKSCDKTHTCPPCPAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 344

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 404

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 464

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 524
```

RESULT 64
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-14

Query Match 46.5%; Score 1257; DB 2; Length 451;
Best Local Similarity 58.4%; Pred. No. 1.3e-89;
Matches 272; Conservative 25; Mismatches 79; Indels 90; Gaps 12;

```
Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|      | |    |    | :  |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
              | ||: : : | |       :|: ||:  | |              ||      |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS--------- 172
              ||   :|: |     |||   :|  |: ||              : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224
```

```
Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 65
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
;  GENERAL INFORMATION:
;    APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;    TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of
;    TITLE OF INVENTION:  Improving Polypeptides
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,352B
;      FILING DATE:  03-Jul-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-887-352B-16

  Query Match             46.5%;  Score 1257;  DB 2;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|      | |    |    | :  |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |            ||      |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS--------- 172
               ||   :|: |     |||   :|  |:  ||           : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                      || ||                 |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 66
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
;  GENERAL INFORMATION:
;    APPLICANT:  Jardieu, Paula M.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,151
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/466163
;      FILING DATE:  06-Jun-1995
;      APPLICATION NUMBER:  08/405617
;      FILING DATE:  15-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/185899
;      FILING DATE:  26-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/879495
;      FILING DATE:  07-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/744768
;      FILING DATE:  14-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-466-151-65
```

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  Query Match           46.5%;  Score 1257;  DB 3;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|     | |   |    | : |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |            ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS--------- 172
              ||   :|: |     |||   :|  |:  ||            : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |   |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 67
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
;  APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;  FILE REFERENCE:  P1123R1
;  CURRENT APPLICATION NUMBER: US/09/109,207C
;  CURRENT FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/051,554
;  PRIOR FILING DATE:  1997-07-03
;  NUMBER OF SEQ ID NOS:  44
; SEQ ID NO 14
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

  Query Match           46.5%;  Score 1257;  DB 3;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|     | |   |    | : |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |            ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS--------- 172
              ||   :|: |     |||   :|  |:  ||            : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |   |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 68
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
;  APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;  FILE REFERENCE:  P1123R1
;  CURRENT APPLICATION NUMBER: US/09/109,207C
;  CURRENT FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/051,554
;  PRIOR FILING DATE:  1997-07-03
;  NUMBER OF SEQ ID NOS:  44
; SEQ ID NO 16
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

  Query Match           46.5%;  Score 1257;  DB 3;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|     | |   |    | : |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |            ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS--------- 172
              ||   :|: |     |||   :|  |:  ||            : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |   |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 69
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
;  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
;  FILE REFERENCE: P1123C1r
;  CURRENT APPLICATION NUMBER: US/09/296,005
;  CURRENT FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 08/887,352
;  EARLIER FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

  Query Match             46.5%;  Score 1257;  DB 3;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |         ::|      | |    |    | :  |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |              ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     |||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 70
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
;  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;  FILE REFERENCE: P1123C1r
;  CURRENT APPLICATION NUMBER: US/09/296,005
;  CURRENT FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 08/887,352
;  EARLIER FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-16

  Query Match             46.5%;  Score 1257;  DB 3;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |         ::|      | |    |    | :  |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |              ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     |||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 71
US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
;  APPLICANT: Lowman, Henry B.
;  APPLICANT:  Presta, Leonard G.
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Lowe, John
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;  FILE REFERENCE: P1123C2US
;  CURRENT APPLICATION NUMBER: US/09/920,171
;  CURRENT FILING DATE:  2001-08-01
;  PRIOR APPLICATION NUMBER: US 08/887,352
;  PRIOR FILING DATE: 1997-07-02
```

```
;  PRIOR APPLICATION NUMBER: US 09/296,005
;  PRIOR FILING DATE: 1999-04-21
;  NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

  Query Match             46.5%;  Score 1257;  DB 4;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|      | |    |    | :  |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |              ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                   || ||                  |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 72
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
;  APPLICANT: Lowman, Henry B.
;  APPLICANT:  Presta, Leonard G.
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Lowe, John
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;  FILE REFERENCE: P1123C2US
;  CURRENT APPLICATION NUMBER: US/09/920,171
;  CURRENT FILING DATE:  2001-08-01
;  PRIOR APPLICATION NUMBER: US 08/887,352
;  PRIOR FILING DATE: 1997-07-02
;  PRIOR APPLICATION NUMBER: US 09/296,005
;  PRIOR FILING DATE: 1999-04-21
;  NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

  Query Match             46.5%;  Score 1257;  DB 4;  Length 451;
  Best Local Similarity   58.4%;  Pred. No. 1.3e-89;
  Matches  272;  Conservative   25;  Mismatches   79;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN--------- 77
              | : | :: |:|  |          ::|      | |    |    | :  |
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: : : | |      :|: ||:  | |              ||       |    :
Db         71 SRDDSKNTFYLQMN------SLRAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                   || ||                  |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 73
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT:  EDELMAN, LENA
;    APPLICANT:  MARGARITTE, CHRISTEL
;    APPLICANT:  KACZOREK, MICHEL
;    APPLICANT:  CHAABIHI, HASSAN
;    TITLE OF INVENTION:  MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,450
;      FILING DATE:  03-MAR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10566
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
```

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;      REFERENCE/DOCKET NUMBER:  660-118-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  472 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-450-8

  Query Match             46.5%;  Score 1257;  DB 4;  Length 472;
  Best Local Similarity   59.0%;  Pred. No. 1.4e-89;
  Matches  268;  Conservative   25;  Mismatches   93;  Indels   68;  Gaps    9;

Qy         32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQ--GSFLTKGPSKLNDRADSRRSL--- 86
              |  :|: ||||        ::|    |    | :  |    | :  |    || ::
Db         32 KPSETLSLTCTVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVD 91

Qy         87 WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
               :  | | : ::   |:  | |    :        :    : |     ||  |:|: |
Db         92 TSKNQFSLKLNSVTAADTAVYYCARAPE--------YKWKYHGDWFDPWGQGTTVTVSSA 143

Qy        147 PGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG 180
                 |||   :|  |:  ||              : ::||                || ||
Db        144 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 203

Qy        181 -----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----P 217
                              |: | |  | |    |:|       |||||||| ||     |
Db        204 LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTQTCPPCPAP 257

Qy        218 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 317

Qy        278 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 337
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        318 EEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 377

Qy        338 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 397
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        378 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPETNYKTTPPVLDSDGSFFLYSKLTV 437

Qy        398 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||
Db        438 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471


RESULT 74
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890001
;  CURRENT APPLICATION NUMBER: US/09/301,593A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107925.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/086,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
;   LENGTH: 472
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-301-593-43

  Query Match             46.5%;  Score 1256.5;  DB 4;  Length 472;
  Best Local Similarity   56.9%;  Pred. No. 1.5e-89;
  Matches  273;  Conservative   38;  Mismatches   86;  Indels   83;  Gaps   15;

Qy         16 LALLPAATQGNKVV-----LGKKGDTVELTCTASQKKSIQF--HWKN---SNQIKILGNQ 65
              ||: | |    ::|     : | | :|:::|  |:    ::  ||       ::: :|
Db         11 LAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIG-- 68

Qy         66 GSFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |     |    | :  | :|           : : :|: ||:  | |         : :
Db         69 GINPNNGIPNYNQKFKGRATLTVGKSASTAYMELSSLRSEDTAVYYC-------ARRRIA 121

Qy        123 FGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------K 167
              :|     : | :   ||   :|: |     |||   :|  |:  ||              :
Db        122 YGY---DEGHAMDYWGQGTLVTVSSST-KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 177

Qy        168 TLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKVEFK 196
              ::||                || ||                |: | |  | |    |
Db        178 PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTK 235

Qy        197 IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
              :|       ||||||||||      ||||||||||||||||||||||||||||||||||
Db        236 VD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 291

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 351

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              |||||||||||||||||||||||||:|:|||||||||||||||||||||||||||||||
Db        352 ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ 411

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471


RESULT 75
US-09-289-942A-7
; Sequence 7, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
;  APPLICANT: Pai, Emil F.
;  APPLICANT:  Klein, Michel H.
;  APPLICANT:  Chong, Pele
;  APPLICANT:  Pedyczak, Arthur
;  TITLE OF INVENTION: Fab'-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODY 2F5
;  FILE REFERENCE: 1038-926 MIS:jb
;  CURRENT APPLICATION NUMBER: US/09/289,942A
;  CURRENT FILING DATE:  1999-04-13
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus type 1
US-09-289-942A-7

  Query Match             46.4%;  Score 1255;  DB 4;  Length 462;
  Best Local Similarity   66.2%;  Pred. No. 1.9e-89;
  Matches  258;  Conservative   18;  Mismatches   52;  Indels   62;  Gaps    9;

Qy         94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-TANSDTHLLQ--GQSLTLTLESPPGSS 150
              |::  :   |: || |            :||:  |    : :   || :|:|: |
Db         82 LVMTRVSPVDTATYFC----AHRRGPTTLFGVPIARGPVNAMDVWGQGITVTISSASTKG 137

Qy        151 PSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG---- 180
              |||   :|  |:  ||              : ::||                || ||
Db        138 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 197
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```
Qy        181 --------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLG 221
                            |: | |  | |    |:|      ||||||||||      |||||
Db        198 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 251

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 311

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        312 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAFPAPIEKTISKAKGQPREPQVYTLPPSRD 371

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 431

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||
Db        432 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 461


RESULT 76
US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
;  APPLICANT: BASEY, CAROL D.
;  APPLICANT:  BLANK, GREG S.
;  TITLE OF INVENTION: PROTEIN PURIFICATION
;  FILE REFERENCE: P1241R1D2
;  CURRENT APPLICATION NUMBER: US/09/679,397
;  CURRENT FILING DATE:  2000-10-03
;  PRIOR APPLICATION NUMBER: US 60/084,459
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: US 09/304,465
;  PRIOR FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

  Query Match             46.4%;  Score 1254.5;  DB 4;  Length 449;
  Best Local Similarity   57.8%;  Pred. No. 2e-89;
  Matches  268;  Conservative   30;  Mismatches   79;  Indels   87;  Gaps   12;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG------SFLTKGPSKLNDRAD 81
              | : | :: |:| ||    |    ||     ::    :|       : | | ::  |
Db         11 LVQPGGSLRLSCAASGFNIKDTYIHW-----VRQAPGKGLEWVARIYPTNGYTRYADSVK 65

Qy         82 SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
                | ::     :    | : :|: ||:  | |                    : :   |
Db         66 GRFTISADTSKNTAYLQMNSLRAEDTAVYYC--------------SRWGGDGFYAMDYWG 111

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |   :|: |     |||   :|  |:  ||             : ::||
Db        112 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 171

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |    |:|       |||||||
Db        172 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 225

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 285

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 345

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        346 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 405

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        406 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 77
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
;  APPLICANT: BASEY, CAROL D.
;  APPLICANT:  BLANK, GREG S.
;  TITLE OF INVENTION: PROTEIN PURIFICATION
;  FILE REFERENCE: P1241R1D1
;  CURRENT APPLICATION NUMBER: US/09/680,148
;  CURRENT FILING DATE:  2000-10-03
;  PRIOR APPLICATION NUMBER: US 60/084,459
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: US 09/304,465
;  PRIOR FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2

  Query Match             46.4%;  Score 1254.5;  DB 4;  Length 449;
  Best Local Similarity   57.8%;  Pred. No. 2e-89;
  Matches  268;  Conservative   30;  Mismatches   79;  Indels   87;  Gaps   12;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG------SFLTKGPSKLNDRAD 81
              | : | :: |:| ||    |    ||     ::    :|       : | | ::  |
Db         11 LVQPGGSLRLSCAASGFNIKDTYIHW-----VRQAPGKGLEWVARIYPTNGYTRYADSVK 65

Qy         82 SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
                | ::     :    | : :|: ||:  | |                    : :   |
Db         66 GRFTISADTSKNTAYLQMNSLRAEDTAVYYC--------------SRWGGDGFYAMDYWG 111

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |   :|: |     |||   :|  |:  ||             : ::||
Db        112 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 171

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |    |:|       |||||||
Db        172 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 225

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 285

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 345

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        346 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 405

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        406 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 78
```

```
US-09-304-465A-2
; Sequence 2, Application US/09304465A
; Patent No. 6489447
; GENERAL INFORMATION:
;  APPLICANT: BASEY, CAROL D.
;  APPLICANT:  BLANK, GREG S.
;  TITLE OF INVENTION: PROTEIN PURIFICATION
;  FILE REFERENCE: P1241R1
;  CURRENT APPLICATION NUMBER: US/09/304,465A
;  CURRENT FILING DATE:  1999-05-03
;  PRIOR APPLICATION NUMBER: US 60/084,459
;  PRIOR FILING DATE: 1998-05-06
;  NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6489447
US-09-304-465A-2

  Query Match             46.4%;  Score 1254.5;  DB 4;  Length 449;
  Best Local Similarity   57.8%;  Pred. No. 2e-89;
  Matches  268;  Conservative   30;  Mismatches   79;  Indels   87;  Gaps   12;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG------SFLTKGPSKLNDRAD 81
              | : | :: |:| ||    |    ||     ::    :|       : | | ::  |
Db         11 LVQPGGSLRLSCAASGFNIKDTYIHW-----VRQAPGKGLEWVARIYPTNGYTRYADSVK 65

Qy         82 SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
              | ::     :    | : :|: ||:  | |                    : :   |
Db         66 GRFTISADTSKNTAYLQMNSLRAEDTAVYYC--------------SRWGGDGFYAMDYWG 111

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |   :|: |      |||   :|  |:  ||            : ::||
Db        112 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 171

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                 |: | |  | |    |:|       |||||||
Db        172 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 225

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 285

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 345

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        346 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 405

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        406 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 79
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,550
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-487-550-4

  Query Match             46.2%;  Score 1248;  DB 3;  Length 476;
  Best Local Similarity   59.2%;  Pred. No. 7e-89;
  Matches  270;  Conservative   26;  Mismatches   86;  Indels   74;  Gaps   13;

Qy         35 DTVELTCTASQKK-SIQFHWKNSNQI---------KILGNQGSFLTKGPSKLNDRADSRR 84
              :|:  ||  |    |  ::|     |           -| || |:     || |  |    :
Db         35 ETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHIYGN-GATTNYNPS-LKSRVTISK 92

Qy         85 SLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLE 144
                 :  | | : ::   |:  | |      : :   : :|   :     : |    :|:
Db         93 DT-SKNQFFLNLNSVTDADTAVYYC-ARGPRPDCTTICYGGWVD-----VWGPGDLVTVS 145

Qy        145 SPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQD 178
              |     |||   :|  |:  ||             : ::||             ||
Db        146 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 205

Qy        179 SG------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC---- 216
              ||                  |: | |  |  |     |:|       ||||||||||
Db        206 SGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCP 259

Qy        217 -PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 275
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 319

Qy        276 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 379

Qy        336 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 439

Qy        396 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||
Db        440 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 80
US-09-526-098-4
; Sequence 4, Application US/09526098
; Patent No. 6492134
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
```

```
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/526,098
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/383,916
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/487,550
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-526-098-4

  Query Match             46.2%;  Score 1248;  DB 4;  Length 476;
  Best Local Similarity   59.2%;  Pred. No. 7e-89;
  Matches  270;  Conservative   26;  Mismatches   86;  Indels   74;  Gaps   13;

Qy         35 DTVELTCTASQKK-SIQFHWKNSNQI---------KILGNQGSFLTKGPSKLNDRADSRR 84
              :|:  ||  |    |  ::|    |           | || |:     || |  |    :
Db         35 ETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHIYGN-GATTNYNPS-LKSRVTISK 92

Qy         85 SLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLE 144
                 : | | : ::   |:  | |     : :   : :|   :     : |    :|:
Db         93 DT-SKNQFFLNLNSVTDADTAVYYC-ARGPRPDCTTICYGGWVD-----VWGPGDLVTVS 145

Qy        145 SPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQD 178
              |     |||   :|  |:  ||             : ::||               ||
Db        146 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 205

Qy        179 SG------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC---- 216
              ||                  |: | |  | |    |:|       ||||||||||
Db        206 SGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCP 259

Qy        217 -PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 275
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 319

Qy        276 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 379

Qy        336 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 439

Qy        396 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||
Db        440 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 81
US-09-313-942-9
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
;  APPLICANT: REGENERON PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;  TITLE OF INVENTION:  AND USING
;  FILE REFERENCE: REG 203-A
;  CURRENT APPLICATION NUMBER: US/09/313,942
;  CURRENT FILING DATE:  1999-05-19
;  PRIOR APPLICATION NUMBER: 09/313,942
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: 60/101,858
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 951
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-313-942-9

  Query Match             45.9%;  Score 1240.5;  DB 4;  Length 951;
  Best Local Similarity   60.4%;  Pred. No. 7.1e-88;
  Matches  265;  Conservative   23;  Mismatches   66;  Indels   85;  Gaps   11;

Qy         70 TKGPSKLNDRADSRRSL--WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ-------- 119
              :|||:    :     ::  |||   |: ::|  | :   :   :   :  |
Db        520 SKGPTVRTKKVGKNEAVLEWDQ--LPVDVQNGFIRNYTIPYRTIIGNETAVNVDSSHTEY 577

Qy        120 ---------LLVFGLTANSDTHLLQGQSLTLTL------ESPPGSS---PSVQCRSPRGK 161
                      | :  : | :|     |   | |       |    |:|   |||   :|  |
Db        578 TLSSLTSDTLYMVRMAAYTDEGGKDGPEFTFTTPKFAQGEIESGASTKGPSVFPLAPSSK 637

Qy        162 NIQGG-------------KTLSVS-------------QLELQDSG--------------- 180
              :  ||               : ::||             || ||
Db        638 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL 697

Qy        181 ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKP 232
                 |: | |  | |     |:|       ||||||||||     ||||||||||||||
Db        698 GTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP 751

Qy        233 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 811

Qy        293 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 871

Qy        353 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 931

Qy        413 MHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||
Db        932 MHEALHNHYTQKSLSLSPG 950


RESULT 82
US-08-472-888A-7
; Sequence 7, Application US/08472888A
; Patent No. 6613746
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian
;    APPLICANT:  Walz, Gerd
;    TITLE OF INVENTION:  AGP-ANTIBODY FUSION PROTEINS
;    TITLE OF INVENTION:  AND RELATED MOLECULES AND METHODS
;    NUMBER OF SEQUENCES:  9
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,888A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/618,314
;      FILING DATE:  23-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/258001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  442 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-472-888A-7

  Query Match             45.8%;  Score 1238;  DB 4;  Length 442;
  Best Local Similarity   74.1%;  Pred. No. 3.8e-88;
  Matches  246;  Conservative   12;  Mismatches   26;  Indels   48;  Gaps    5;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS---------- 172
              ||   :|: |      |||   :|  |:  ||              : ::||
Db        122 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181

Qy        173 ---QLELQDSGTWTCTVL-----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL 219
                  || || :: : :      : |||           ||||||||||     |||
Db        182 HTFPAVLQSSGLYSLSSVVTVPSSSDKKV------------EPKSCDKTHTCPPCPAPEL 229

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 289

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 349

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 409

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        410 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 83
PCT-US96-10043-9
; Sequence 9, Application PC/TUS9610043
;  GENERAL INFORMATION:
;    APPLICANT:  The General Hospital Corporation
;    TITLE OF INVENTION:  P-SELECTIN LIGANDS AND RELATED MOLECULES
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,213
;      FILING DATE:  14-JUN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  00786/284001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  442 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-10043-9

  Query Match             45.8%;  Score 1238;  DB 5;  Length 442;
  Best Local Similarity   74.1%;  Pred. No. 3.8e-88;
  Matches  246;  Conservative   12;  Mismatches   26;  Indels   48;  Gaps    5;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS---------- 172
              ||   :|: |      |||   :|  |:  ||              : ::||
Db        122 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181

Qy        173 ---QLELQDSGTWTCTVL-----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL 219
                  || || :: : :      : |||           ||||||||||     |||
Db        182 HTFPAVLQSSGLYSLSSVVTVPSSSDKKV------------EPKSCDKTHTCPPCPAPEL 229

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 289

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 349

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 409

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        410 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 84
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
```

```
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. 6610286ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-54

  Query Match             45.8%;  Score 1238;  DB 4;  Length 547;
  Best Local Similarity   58.8%;  Pred. No. 5.1e-88;
  Matches  276;  Conservative   23;  Mismatches   72;  Indels   98;  Gaps   15;

Qy          27 KVVLGKKGDTVELTCTASQKKSIQFHWK-NSNQIKILGNQ-GSFLTKGPSKLNDRADSRR 84
               :| |      :: :  || :|       || |   : :    |  | |     | || :::
Db         112 EVALTTDEKSISVVLTAPEK------WKRNPEDLPVSMQQIYSNLKYNVSVLNTKSN--- 162

Qy          85 SLWDQ--GNFPLIIKNLKIEDSDTYICEVED---------QKEEVQLLVFGLTANSDTHL 133
                 | |    |  |::  |  | :  |   ||           |  | |
Db         163 RTWSQCVTNHTLVLTWL--EPNTLYCVHVESFVPGPPRRAQPSEKQC------------- 207

Qy         134 LQGQSLTLTLESPPGSS--PSVQCRSPRGKNIQGG------------KTLSVS------ 172
                : ||  :|   |:  |||   :|  |:  ||             : ::||
Db         208 ----ARTLKDQSSEASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 263

Qy         173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                     || ||                    |: | |  | |    |:|       ||
Db         264 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEP 317

Qy         208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
               |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db         318 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 377

Qy         263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         378 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 437

Qy         323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         438 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 497

Qy         383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db         498 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 546


RESULT 85
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. 6610286ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 53
;   LENGTH: 571
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-53

  Query Match             45.8%;  Score 1238;  DB 4;  Length 571;
  Best Local Similarity   58.8%;  Pred. No. 5.4e-88;
  Matches  276;  Conservative   23;  Mismatches   72;  Indels   98;  Gaps   15;

Qy          27 KVVLGKKGDTVELTCTASQKKSIQFHWK-NSNQIKILGNQ-GSFLTKGPSKLNDRADSRR 84
               :| |      :: :  || :|       || |   : :    |  | |     | || :::
Db         136 EVALTTDEKSISVVLTAPEK------WKRNPEDLPVSMQQIYSNLKYNVSVLNTKSN--- 186

Qy          85 SLWDQ--GNFPLIIKNLKIEDSDTYICEVED---------QKEEVQLLVFGLTANSDTHL 133
                 | |    |  |::  |  | :  |   ||           |  | |
Db         187 RTWSQCVTNHTLVLTWL--EPNTLYCVHVESFVPGPPRRAQPSEKQC------------- 231

Qy         134 LQGQSLTLTLESPPGSS--PSVQCRSPRGKNIQGG------------KTLSVS------ 172
                : ||  :|   |:  |||   :|  |:  ||             : ::||
Db         232 ----ARTLKDQSSEASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 287

Qy         173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                     || ||                    |: | |  | |    |:|       ||
Db         288 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEP 341

Qy         208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
               |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db         342 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 401

Qy         263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         402 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 461

Qy         323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         462 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 521

Qy         383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db         522 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 570


RESULT 86
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
```

```
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/236,311
;       FILING DATE:  02-MAY-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/936190
;       FILING DATE:  26-AUG-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/842777
;       FILING DATE:  18-FEB-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/250785
;       FILING DATE:  28-SEP-1988
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/104329
;       FILING DATE:  02-OCT-1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hasak, Janet E.
;       REGISTRATION NUMBER:  28,616
;       REFERENCE/DOCKET NUMBER:  444P1C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-1896
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  371 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-236-311-7

  Query Match             45.8%;  Score 1236.5;  DB 1;  Length 371;
  Best Local Similarity   72.2%;  Pred. No. 3.9e-88;
  Matches  249;  Conservative    9;  Mismatches   32;  Indels   55;  Gaps    6;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS---------- 172
              |    :|: |     |||   :|  |:  ||            : ::||
Db         32 GLGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 91

Qy        173 ---QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211
                 || ||                   |: | |  | |     |:|       ||||||
Db         92 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD 145

Qy        212 KTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 266
              |||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 205

Qy        267 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 265

Qy        327 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 325

Qy        387 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        326 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 370


RESULT 87
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  371 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-457-918-7

  Query Match             45.8%;  Score 1236.5;  DB 3;  Length 371;
  Best Local Similarity   72.2%;  Pred. No. 3.9e-88;
  Matches  249;  Conservative    9;  Mismatches   32;  Indels   55;  Gaps    6;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS---------- 172
              |    :|: |     |||   :|  |:  ||            : ::||
Db         32 GLGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 91

Qy        173 ---QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211
                 || ||                   |: | |  | |     |:|       ||||||
Db         92 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD 145

Qy        212 KTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 266
              |||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 205

Qy        267 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 265

Qy        327 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 325

Qy        387 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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              ||||||||||||||||||||||||||||||||||||||||||||
Db        326 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 370


RESULT 88
US-09-157-452B-12
; Sequence 12, Application US/09157452B
; Patent No. 6482409
; GENERAL INFORMATION:
;  APPLICANT: Lobb, Roy R.
;  APPLICANT:  Burkly, Linda C.
;  TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
;  FILE REFERENCE: 10274-004003
;  CURRENT APPLICATION NUMBER: US/09/157,452B
;  CURRENT FILING DATE:  1998-09-21
;  PRIOR APPLICATION NUMBER: US 08/950,660
;  PRIOR FILING DATE: 1997-10-15
;  PRIOR APPLICATION NUMBER: US 08/373,857
;  PRIOR FILING DATE: 1995-01-18
;  PRIOR APPLICATION NUMBER: US 08/284,603
;  PRIOR FILING DATE: 1994-08-11
;  PRIOR APPLICATION NUMBER: PCT/US93/00924
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: US 07/835,139
;  PRIOR FILING DATE: 1992-02-12
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-157-452B-12

  Query Match             45.7%;  Score 1234.5;  DB 4;  Length 446;
  Best Local Similarity   57.3%;  Pred. No. 7.1e-88;
  Matches  270;  Conservative   36;  Mismatches   70;  Indels   95;  Gaps   15;

Qy         16 LALLPAATQGNKV-------VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILG---NQ 65
              | :: ||:|  |:        | : ||:| |||: :  :|  | |:       : |   |:
Db         15 LWIMFAASQAFKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNE 74

Qy         66 G--SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV--EDQKEE--VQ 119
              |  | ||  |                          :  :  :|:|    | :| |  :|
Db         75 GTTSTLTMNP------------------------VSFGNEHSYLCTATCESRKLEKGIQ 109

Qy        120 LLVFGLTANSDTHLLQGQSLTLTLESPP---GSSPSVQCRSP------------RGKNI 163
              : ::    : : ||           | |   |   :|:|                :| ::
Db        110 VEIYSFPKDPEIHL-----------SGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHL 158

Qy        164 QGG---------KTLSVSQLE------LQDSGTWTCTVLQNQKKVEF-KIDIVPC--PAP 205
                 |:|    ||      ::| |      ||  : |:   ::| ||     |
Db        159 MKSQEFLEDADRKSLETKSLEVTFTPVIEDIG----KVLVCRAKLHIDEMDSVPTVRQAV 214

Qy        206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
              :    ||||||     ||||||||||||||||||||||||||||||||||||||||||||
Db        215 KELQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 274

Qy        261 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 334

Qy        321 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 394

Qy        381 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 445


RESULT 89
US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
;  APPLICANT:  Cerretti, Douglas P.
;  APPLICANT:  Borges, Luis G.
;  APPLICANT:  Fanslow, III, William C.
;  TITLE OF INVENTION:  TEK ANTAGONISTS
;  FILE REFERENCE:  2900-A
;  CURRENT APPLICATION NUMBER: US/09/590,656
;  CURRENT FILING DATE:  2000-06-07
;  PRIOR APPLICATION NUMBER:  60/137,889
;  PRIOR FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 704
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-590-656-2

  Query Match             45.6%;  Score 1232;  DB 4;  Length 704;
  Best Local Similarity   82.5%;  Pred. No. 2.1e-87;
  Matches  236;  Conservative    4;  Mismatches   14;  Indels   32;  Gaps    3;

Qy        178 DSGTWTCTVLQNQKKVE--FKIDIVPCPAP-------------------------EPKSC 210
              ||| | |:|       ||  | | :   | |                         |||||
Db        418 DSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGEPKSC 477

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 537

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 597

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              |||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Db        598 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 657

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        658 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 703


RESULT 90
US-09-733-764-2
; Sequence 2, Application US/09733764
; Patent No. 6521424
; GENERAL INFORMATION:
;  APPLICANT: Cerretti, Douglas P.
;  APPLICANT:  Borges, Luis G.
;  APPLICANT:  Fanslow, III, William C.
;  TITLE OF INVENTION: TEK ANTAGONISTS
;  FILE REFERENCE: 2900-A
;  CURRENT APPLICATION NUMBER: US/09/733,764
;  CURRENT FILING DATE:  2000-12-07
;  PRIOR APPLICATION NUMBER: 09/590,656
;  PRIOR FILING DATE: 1999-06-07
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 704
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-733-764-2

  Query Match             45.6%;  Score 1232;  DB 4;  Length 704;
  Best Local Similarity   82.5%;  Pred. No. 2.1e-87;
  Matches  236;  Conservative    4;  Mismatches   14;  Indels   32;  Gaps    3;

Qy        178 DSGTWTCTVLQNQKKVE--FKIDIVPCPAP-------------------------EPKSC 210
              ||| | |:|       ||  | | :   | |                         |||||
Db        418 DSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGEPKSC 477
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Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 537

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 597

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        598 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 657

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        658 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 703


RESULT 91
US-08-461-968A-5
; Sequence 5, Application US/08461968A
; Patent No. 5801044
;  GENERAL INFORMATION:
;    APPLICANT:  Seed et al., Brian
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE INTERACTIONS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  0210-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,968A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/618,314
;      FILING DATE:  23-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/067003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  442 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-968A-5

  Query Match             45.4%;  Score 1226;  DB 1;  Length 442;
  Best Local Similarity   73.5%;  Pred. No. 3.2e-87;
  Matches  244;  Conservative   12;  Mismatches   28;  Indels   48;  Gaps    5;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS---------- 172
              ||   :|: |     |||   :|  |:  ||             : ::||
Db        122 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181

Qy        173 ---QLELQDSGTWTCTVL-----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL 219
                  || || :: : :      : |||           ||||||||||     |||
Db        182 HTFPAVLQSSGLYSLSSVVTVPSSSDKKV-----------EPKSCDKTHTCPPCPAPEL 229

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        230 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHRNKTKPREE 289

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 349

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 409

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        410 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 92
US-08-462-571-5
; Sequence 5, Application US/08462571
; Patent No. 5858983
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian et al.
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE INTERACTIONS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,571
;      FILING DATE:  05 June 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/618,314
;      FILING DATE:  23 No. 5858983ember 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/067002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  442 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-571-5

  Query Match             45.4%;  Score 1226;  DB 2;  Length 442;
  Best Local Similarity   73.5%;  Pred. No. 3.2e-87;
  Matches  244;  Conservative   12;  Mismatches   28;  Indels   48;  Gaps    5;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS---------- 172
              ||   :|: |     |||   :|  |:  ||             : ::||
Db        122 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181

Qy        173 ---QLELQDSGTWTCTVL-----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL 219
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                 || ||  :: : :        : |||             ||||||||||     |||
Db        182 HTFPAVLQSSGLYSLSSVVTVPSSSDKKV------------EPKSCDKTHTCPPCPAPEL 229

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        230 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHRNKTKPREE 289

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 349

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 409

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        410 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441
```

RESULT 93
PCT-US96-10043-11
; Sequence 11, Application PC/TUS9610043
; GENERAL INFORMATION:
;   APPLICANT: The General Hospital Corporation
;   TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
;   TITLE OF INVENTION: AND METHODS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02210-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/10043
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/000,213
;   FILING DATE: 14-JUN-1995
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lech, Karen F.
;   REGISTRATION NUMBER:
;   REFERENCE/DOCKET NUMBER: 00786/284001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 437 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US96-10043-11

```
  Query Match             45.3%;  Score 1224;  DB 5;  Length 437;
  Best Local Similarity   72.3%;  Pred. No. 4.5e-87;
  Matches  250;  Conservative   16;  Mismatches   38;  Indels   42;  Gaps    8;

Qy         99 LKIEDSDTYIC--EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQC- 155
              | : |: ||:  :| |:|          :||:  :|       :     |        :: |
Db        120 LILRDTKTYMLAFDVNDEKN------WGLSVYADKPETTKEQLGEFYE-------ALDCL 166

Qy        156 RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQ-----KKVEFKIDIVPCPAPEPKSC 210
              | |:           | :    |    |  |: |     |: | : |     |  |||||
Db        167 RIPK-----------SDVVYTDWKKDKCEPLEKQHEKERKQEEGESD----PEGEPKSC 210

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     |||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 270

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 330

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 390

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        391 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 436
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RESULT 94
US-09-301-593-22
; Sequence 22, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-301-593-22

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  Query Match             45.2%;  Score 1221.5;  DB 4;  Length 330;
  Best Local Similarity   73.9%;  Pred. No. 4.8e-87;
  Matches  244;  Conservative    9;  Mismatches   22;  Indels   55;  Gaps    6;

Qy        151 PSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG---- 180
              |||   :|  |:  ||                 : ::||                || ||
Db          6 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 65

Qy        181 --------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLG 221
                            |: |  |  |      |:|      ||||||||||      |||||
Db         66 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 119

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 179

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        180 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 239

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 299

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                 ||||||||||||||||||||||||||||||
Db        300 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 329


RESULT 95
US-09-313-942-8
; Sequence 8, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
;  APPLICANT: REGENERON PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;  TITLE OF INVENTION:  AND USING
;  FILE REFERENCE: REG 203-A
;  CURRENT APPLICATION NUMBER: US/09/313,942
;  CURRENT FILING DATE:  1999-05-19
;  PRIOR APPLICATION NUMBER: 09/313,942
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: 60/101,858
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 592
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-313-942-8

  Query Match             45.2%;  Score 1221;  DB 4;  Length 592;
  Best Local Similarity   80.5%;  Pred. No. 1.2e-86;
  Matches  236;  Conservative   10;  Mismatches   22;  Indels   25;  Gaps    3;

Qy        150 SPSVQCRSPRGKNIQGGKTLSVS------QLELQDSGTWTCTVLQNQKKVEFKIDIVPCP 203
              :|  : |||  :|       :::       :  :||   |   :|:
Db        313 TPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQD-------------- 358

Qy        204 APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 258
              | ||||||||||||     ||||||||||||||||||||||||||||||||||||||||
Db        359 AGEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 418

Qy        259 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 478

Qy        319 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 538

Qy        379 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 591


RESULT 96
PCT-US95-03866-12
; Sequence 12, Application PC/TUS9503866
;  GENERAL INFORMATION:
;    APPLICANT:  CytoMed, Inc. (all states except US)
;    APPLICANT:  Nocka, Karl (US only)
;    APPLICANT:  Lobell, Robert B (US only)
;    TITLE OF INVENTION:  STABILIZED DIMER OF KIT LIGAND AND
;    TITLE OF INVENTION:  FLT-3/FLK-2 LIGAND
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03866
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,379
;      FILING DATE:  28-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  CytoMed/2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-596-9000
;      TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  424 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-03866-12

  Query Match             45.1%;  Score 1219;  DB 5;  Length 424;
  Best Local Similarity   66.8%;  Pred. No. 1.1e-86;
  Matches  253;  Conservative   18;  Mismatches   48;  Indels   60;  Gaps    9;

Qy         80 ADSRRSLWDQ--------GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              :||   | |:         |: :| | : | | |   |  |:  ::::
Db         78 SDSLTDLLDKFSNISEGLSNYSIIDKLVNIVD-DLVECVKENSSKDLK------------ 124

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPR------GKNIQGGKTLSVSQLELQDSGTWTCT 185
                                ||  :  :|      ::|   |   |:     | | |
Db        125 --------------KSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVA------SETSDCV 164

Qy        186 V---LQNQKKVEFKID----IVPCPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKP 232
              |   |  :|      :     : |  | ||||||||||||     ||||||||||||||||
Db        165 VSSTLSPEKDSRVSVTKPFMLPPVAADPEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP 224

Qy        233 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 284

Qy        293 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 344

Qy        353 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 404

Qy        413 MHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||
Db        405 MHEALHNHYTQKSLSLSPG 423


RESULT 97
PCT-US95-03866-14
; Sequence 14, Application PC/TUS9503866
;  GENERAL INFORMATION:
;    APPLICANT:  CytoMed, Inc. (all states except US)
;    APPLICANT:  Nocka, Karl (US only)
;    APPLICANT:  Lobell, Robert B (US only)
;    TITLE OF INVENTION:  STABILIZED DIMER OF KIT LIGAND AND
;    TITLE OF INVENTION:  FLT-3/FLK-2 LIGAND
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03866
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,379
;      FILING DATE:  28-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  CytoMed/2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-596-9000
;      TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  424 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-03866-14

  Query Match             45.1%;  Score 1219;  DB 5;  Length 424;
  Best Local Similarity   66.8%;  Pred. No. 1.1e-86;
  Matches  253;  Conservative   18;  Mismatches   48;  Indels   60;  Gaps    9;

Qy         80 ADSRRSLWDQ--------GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              :||   | |:         |: :| | : | | |   |  |:  ::::
Db         78 SDSLTDLLDKFSNISEGLSNYSIIDKLVNIVD-DLVECVKENSSKDLK------------ 124

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPR------GKNIQGGKTLSVSQLELQDSGTWTCT 185
                          ||  :  :|       ::|   |   |:      | |  |
Db        125 --------------KSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVA------SETSDCV 164

Qy        186 V---LQNQKKVEFKID----IVPCPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKP 232
              |   | :|     :     : |  | ||||||||||||     ||||||||||||||||
Db        165 VSSTLSPEKDSRVSVTKPFMLPPVAADPEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP 224

Qy        233 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 284

Qy        293 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 344

Qy        353 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 404

Qy        413 MHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||
Db        405 MHEALHNHYTQKSLSLSPG 423


RESULT 98
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, No. 6306395io
;  APPLICANT: NAGATA, Shigekazu
;  TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
;  FILE REFERENCE: 1110-207P
;  CURRENT APPLICATION NUMBER: US/09/180,100
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: PCT/JP97/01502
;  EARLIER FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-180-100-11

  Query Match             45.0%;  Score 1215;  DB 4;  Length 360;
  Best Local Similarity   91.3%;  Pred. No. 1.7e-86;
  Matches  231;  Conservative    2;  Mismatches   10;  Indels   10;  Gaps    2;

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              ||:  | |  |          : ||||||||||     ||||||||||||||||||||
Db        112 CTLTSNTKCKE-----EGSRSNEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 166

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 226

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 286

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 346

Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
Db        347 NHYTQKSLSLSPG 359


RESULT 99
US-09-180-100-22
; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, No. 6306395io
;  APPLICANT: NAGATA, Shigekazu
;  TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
;  FILE REFERENCE: 1110-207P
;  CURRENT APPLICATION NUMBER: US/09/180,100
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: PCT/JP97/01502
;  EARLIER FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 376
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-180-100-22

  Query Match             45.0%;  Score 1215;  DB 4;  Length 376;
  Best Local Similarity   91.3%;  Pred. No. 1.8e-86;
  Matches  231;  Conservative    2;  Mismatches   10;  Indels   10;  Gaps    2;

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              ||:  | |  |          : ||||||||||     ||||||||||||||||||||
Db        128 CTLTSNTKCKE-----EGSRSNEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 182

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 242

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 302

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 362
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Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
Db        363 NHYTQKSLSLSPG 375


RESULT 100
US-09-333-593A-8
; Sequence 8, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
;  APPLICANT:  DEEN, KEITH C.
;  APPLICANT:  YOUNG, PETER R.
;  APPLICANT:  MARSHALL, LISA A.
;  APPLICANT:  ROSHAK, AMY K.
;  APPLICANT:  TAN, KONG B.
;  APPLICANT:  TRUNEH, ALEMSEGED
;  TITLE OF INVENTION:  TUMOR NECROSIS FACTOR RELATED RECEPTOR,
;  TITLE OF INVENTION:  TR6
;  FILE REFERENCE:  GH-50008-2
;  CURRENT APPLICATION NUMBER: US/09/333,593A
;  CURRENT FILING DATE:  1999-06-15
;  PRIOR APPLICATION NUMBER:  08/916,625
;  PRIOR FILING DATE:  1997-08-22
;  PRIOR APPLICATION NUMBER:  08/853,684
;  PRIOR FILING DATE:  1997-05-09
;  PRIOR APPLICATION NUMBER:  60/041,230
;  PRIOR FILING DATE:  1997-03-14
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-333-593A-8

  Query Match             45.0%;  Score 1215;  DB 4;  Length 424;
  Best Local Similarity   74.6%;  Pred. No. 2.2e-86;
  Matches  241;  Conservative   14;  Mismatches   38;  Indels   30;  Gaps    5;

Qy        117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
              ||:|     | |:   : | :  |   |  |      :   |||          :::
Db        123 EVELSPCTTTRNT---VCQCEEGTFREEDSPEMCRKCRTGCPRG-----------MVKV 167

Qy        177 QDSGTWT---CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLF 228
               |   |:   |   :: : :| :         |||| ||||||     ||||||||||||
Db        168 GDCTPWSDIECVHKESGRSIEGR-------GTEPKSADKTHTCPPCPAPELLGGPSVFLF 220

Qy        229 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 280

Qy        289 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV 340

Qy        349 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 400

Qy        409 SCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||
Db        401 SCSVMHEALHNHYTQKSLSLSPG 423


Search completed: August  3, 2004, 13:17:18
Job time : 22.0673 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 3, 2004, 13:14:00 ; Search time 43.3363 Seconds
(without alignments)
3706.029 Million cell updates/sec

Title: SEQ8
Perfect score: 2702
Sequence: 1 MNRGVPFRHLLLVLQLALLP.....VISFLLGLGLGVACVLARTR 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 125 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2122	78.5	432	8	US-08-485-163-3	Sequence 3, Appli
2	2122	78.5	432	9	US-09-766-995-2	Sequence 2, Appli
3	2085	77.2	530	8	US-08-485-163-5	Sequence 5, Appli
4	2085	77.2	530	9	US-09-766-995-4	Sequence 4, Appli
5	1338.5	49.5	254	10	US-09-939-537-33	Sequence 33, Appl
6	1291.5	47.8	465	12	US-10-404-724-8	Sequence 8, Appli
7	1289	47.7	713	16	US-10-679-620-64	Sequence 64, Appl
8	1289	47.7	715	16	US-10-679-620-62	Sequence 62, Appl
9	1287.5	47.6	437	14	US-10-363-427-14	Sequence 14, Appl
10	1285.5	47.6	663	12	US-10-412-406-32	Sequence 32, Appl
11	1285.5	47.6	4852	12	US-10-412-406-33	Sequence 33, Appl
12	1282.5	47.5	446	12	US-10-435-299-7	Sequence 7, Appli
13	1282.5	47.5	617	14	US-10-363-427-18	Sequence 18, Appl
14	1282.5	47.5	617	14	US-10-363-427-22	Sequence 22, Appl
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19	1280	47.4	476	9	US-09-747-669-3	Sequence 3, Appli
20	1280	47.4	476	14	US-10-290-703-3	Sequence 3, Appli
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23	1277.5	47.3	470	15	US-10-108-260A-4292	Sequence 4292, Ap
24	1277	47.3	543	14	US-10-207-655-345	Sequence 345, App
25	1276.5	47.2	475	9	US-09-740-002-25	Sequence 25, Appl
26	1276.5	47.2	475	16	US-10-325-698-25	Sequence 25, Appl
27	1275.5	47.2	579	14	US-10-138-727A-41	Sequence 41, Appl
28	1275	47.2	600	16	US-10-334-235-38	Sequence 38, Appl
29	1274.5	47.2	445	14	US-10-320-231A-79	Sequence 79, Appl
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31	1273.5	47.1	444	16	US-10-704-522-6	Sequence 6, Appli
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35	1273.5	47.1	497	12	US-10-683-255-6	Sequence 6, Appli
36	1273.5	47.1	525	12	US-10-683-255-4	Sequence 4, Appli
37	1273.5	47.1	622	12	US-10-683-255-2	Sequence 2, Appli
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39	1272	47.1	476	16	US-10-660-128-12	Sequence 12, Appl
40	1271.5	47.1	453	14	US-10-159-006-18	Sequence 18, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/08485163
; Publication No. US20020098191A1
;  GENERAL INFORMATION:
;    APPLICANT:  Beaudry, Gary A.
;    APPLICANT:  Maddon, Paul J.
;    TITLE OF INVENTION:  CD4-GAMMA2 CD4-IgG2 CHIMERAS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,163
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  37690-II-1-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      CELL TYPE:  lymphocyte
US-08-485-163-3

  Query Match             78.5%;  Score 2122;  DB 8;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 2e-134;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

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Qy        181 TWTCTVLQNQKKVEFKIDIV------------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
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Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
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Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
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Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
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Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 2
US-09-766-995-2
; Sequence 2, Application US/09766995
; Patent No. US20020052481A1
; GENERAL INFORMATION:
;  APPLICANT: Graham P. Allaway et al.
;  TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 2048/41215-CB/JPW/SHS
;  CURRENT APPLICATION NUMBER: US/09/766,995
;  CURRENT FILING DATE:  2001-01-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: homo sapians
US-09-766-995-2

  Query Match             78.5%;  Score 2122;  DB 9;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 2e-134;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;
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Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
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Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
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Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
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Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
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Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
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Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 3
US-08-485-163-5
; Sequence 5, Application US/08485163
; Publication No. US20020098191A1
;  GENERAL INFORMATION:
;    APPLICANT:  Beaudry, Gary A.
;    APPLICANT:  Maddon, Paul J.
;    TITLE OF INVENTION:  CD4-GAMMA2 CD4-IgG2 CHIMERAS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,163
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  37690-II-1-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  530 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      CELL TYPE:  lymphocyte
US-08-485-163-5

  Query Match           77.2%;  Score 2085;  DB 8;  Length 530;
  Best Local Similarity  77.3%;  Pred. No. 7.9e-132;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              |||||||||||||||||||                ||                  |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : ||||||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||:|||:||||||||:|||||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 4
US-09-766-995-4
; Sequence 4, Application US/09766995
; Patent No. US20020052481A1
; GENERAL INFORMATION:
;  APPLICANT: Graham P. Allaway et al.
;  TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCON
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 2048/41215-CB/JPW/SHS
;  CURRENT APPLICATION NUMBER: US/09/766,995
;  CURRENT FILING DATE:  2001-01-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 530
;   TYPE: PRT
;   ORGANISM: homo sapians
US-09-766-995-4

  Query Match           77.2%;  Score 2085;  DB 9;  Length 530;
  Best Local Similarity  77.3%;  Pred. No. 7.9e-132;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
```

```
Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA-----------------PEP 207
              ||||||||||||||||||||                ||                  |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : ||||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||:|||:||||||||:|||||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 5
US-09-939-537-33
; Sequence 33, Application US/09939537
; Publication No. US20030138410A1
;  GENERAL INFORMATION:
;       APPLICANT: Seed, Brian
;                  Banapour, Babak
;                  Romeo, Charles
;                  Kolanus, Waldemar
;       TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
;                           CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
;       NUMBER OF SEQUENCES: 53
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Clark & Elbing LLP
;            STREET: 176 Federal Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02110
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/939,537
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/284,391
;            FILING DATE: 02-AUG-1994
;            APPLICATION NUMBER: 08/195,395
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: 07/847,566
;            FILING DATE: 06-MAR-1992
;            APPLICATION NUMBER: 07/665,961
;            FILING DATE: 07-MAR-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Elbing, Karen L
;            REGISTRATION NUMBER: 35,238
;            REFERENCE/DOCKET NUMBER: 00786/247001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617-428-0200
;            TELEFAX: 617-428-7045
;            TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 33:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 254 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-939-537-33

  Query Match             49.5%;  Score 1338.5;  DB 10;  Length 254;
  Best Local Similarity   98.0%;  Pred. No. 4.7e-82;
  Matches  249;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    1;

Qy        206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
              |||||||||||     |||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy        261 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        321 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        381 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 240

Qy        441 AQDGELDGLWTTDP 454
              ||||||||||||||
Db        241 AQDGELDGLWTTDP 254


RESULT 6
US-10-404-724-8
; Sequence 8, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
;  APPLICANT: Horwitz, Arnold H.
;  TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 13698US01
;  CURRENT APPLICATION NUMBER: US/10/404,724
;  CURRENT FILING DATE:  2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/368,530
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-404-724-8

  Query Match             47.8%;  Score 1291.5;  DB 12;  Length 465;
  Best Local Similarity   58.1%;  Pred. No. 1.4e-78;
  Matches  286;  Conservative   23;  Mismatches   78;  Indels  105;  Gaps   13;

Qy         11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG 66
              || |  |   |  |   |  |    | |:||:::| ||       |     | :|   :|
Db          7 LLFLMAAAQSAQAQIQLVQSGPELKKPGETVKISCKAS---GYTFTKYGMNWVKQAPGKG 63

Qy         67 -------SFLTKGPSKLNDRADSRRSLWDQGNFP----------LIIKNLKIEDSDTYI 108
                    :  |: |:  :|         :| |          | | ||| ||: ||
Db         64 LKWMGWINTYTEEPTYGDD---------FKGRFAFSLETSASTANLQINNLKSEDTATYF 114
```

```
Qy        109 CEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
Db        115 C-----------ARFGSAVD-----YWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA 158

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
Db        159 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 218

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
Db        219 NV--NHKPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 272

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
Db        273 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 332

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
Db        333 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 392

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
Db        393 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 452

Qy        420 HYTQKSLSLSPG 431
Db        453 HYTQKSLSLSPG 464
```

RESULT 7
US-10-679-620-64
; Sequence 64, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p9E10chimericv2-1, see Example 15
US-10-679-620-64

Query Match 47.7%; Score 1289; DB 16; Length 713;
Best Local Similarity 59.3%; Pred. No. 3.6e-78;
Matches 275; Conservative 28; Mismatches 81; Indels 80; Gaps 11;

```
Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL 76
Db        267 LVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEW-----VATIGSRGTY-THYPDSV 320

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
Db        321 KGRFTISRDN-DKNALYLQMNSLKSEDTAMYYC-----ARRSEFYYYGNTYYYSAMDYWG 374

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
Db        375 QGASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 434

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
Db        435 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK 488

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
Db        489 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 548

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
Db        549 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 608

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
Db        609 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 668

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        669 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 712
```

RESULT 8
US-10-679-620-62
; Sequence 62, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p9E10chimericv1-1, see Example 15
US-10-679-620-62

Query Match 47.7%; Score 1289; DB 16; Length 715;
Best Local Similarity 59.3%; Pred. No. 3.7e-78;
Matches 275; Conservative 28; Mismatches 81; Indels 80; Gaps 11;

```
Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL 76
Db        269 LVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEW-----VATIGSRGTY-THYPDSV 322

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
Db        323 KGRFTISRDN-DKNALYLQMNSLKSEDTAMYYC-----ARRSEFYYYGNTYYYSAMDYWG 376

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
Db        377 QGASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 436

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
Db        437 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK 490

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
Db        491 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 550

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
Db        551 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 610

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
Db        611 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 670
```

```
Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||
Db        671 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 714


RESULT 9
US-10-363-427-14
; Sequence 14, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
;  APPLICANT: MeDexGen Inc.
;  APPLICANT:  CHUNG, Yong Hoon
;  APPLICANT:  HAN, Ji Woong
;  APPLICANT:  LEE, Hye Ja
;  APPLICANT:  CHOI, Eun Yong
;  APPLICANT:  KIM, Jin Mi
;  APPLICANT:  YIM, Soo Bin
;  TITLE OF INVENTION: Concatametric Immunoadhesion
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/363,427
;  CURRENT FILING DATE:  2003-02-28
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 14
;   LENGTH: 437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-363-427-14

  Query Match             47.6%;  Score 1287.5;  DB 14;  Length 437;
  Best Local Similarity   64.7%;  Pred. No. 2.5e-78;
  Matches  273;  Conservative   22;  Mismatches   62;  Indels   65;  Gaps   11;

Qy         35 DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL 94
              | ::   |: :||  ||  :           :|  |   ||             | |
Db         55 DDIKWEKTSDKKKIAQFRKEKE----------TFKEKDTYKLFK-----------NGTL 92

Qy         95 IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ-----------SLTLT 142
              ||:|| :| | |   : | | : |   :| |        :| :           : |||
Db         93 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-------IQERVSKPKISWTCINTTLT 145

Qy        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT--------CTVLQNQKKVE 194
              |   |: | :           | || | :||  :  :  ||         ||   |:   |
Db        146 CEVMNGTDPELNL-------YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 195

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
              :: | ||| ||||||||||      ||||||||||||||||||||||||||||||||
Db        196 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 254

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 314

Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 374

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 434

Qy        430 PG 431
              ||
Db        435 PG 436


RESULT 10
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  APPLICANT:  GARBER, Ellen
;  APPLICANT:  LYNE, Paul
;  APPLICANT:  SALDHANA, Jose W.
;  TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
;  FILE REFERENCE: BINA100CN
;  CURRENT APPLICATION NUMBER: US/10/412,406
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: 60/240,285
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: 60/275,289
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: 60/299,987
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: PCT/US01/32140
;  PRIOR FILING DATE: 2001-10-12
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 663
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-412-406-32

  Query Match             47.6%;  Score 1285.5;  DB 12;  Length 663;
  Best Local Similarity   59.0%;  Pred. No. 5.7e-78;
  Matches  275;  Conservative   29;  Mismatches   71;  Indels   91;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFLTKGPSKLN---- 77
              | | | :: |:| ||          :|       |    :  : : ||: | |  |  :
Db        225 LVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSY-TYYPDSVKGRFT 283

Qy         78 -DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ- 135
              | ::: ||:       | : :|: ||:  | |  |:                 | : :
Db        284 ISRDNAKNSLY------LQMSSLRAEDTAVYYCAREE-------------NGNFYYFDY 323

Qy        136 -GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||  |:|: |     |||   :|  |: ||             : ::||
Db        324 WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 383

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                  |: | |  | |    |:|       |||||
Db        384 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 437

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 497

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 557

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 617

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        618 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 663


RESULT 11
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  APPLICANT:  GARBER, Ellen
;  APPLICANT:  LYNE, Paul
;  APPLICANT:  SALDHANA, Jose W.
;  TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
;  FILE REFERENCE: BINA100CN
;  CURRENT APPLICATION NUMBER: US/10/412,406
;  CURRENT FILING DATE:  2003-04-10
```

```
;  PRIOR APPLICATION NUMBER: 60/240,285
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: 60/275,289
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: 60/299,987
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: PCT/US01/32140
;  PRIOR FILING DATE: 2001-10-12
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 4852
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-412-406-33

  Query Match             47.6%;  Score 1285.5;  DB 12;  Length 4852;
  Best Local Similarity   59.0%;  Pred. No. 7e-77;
  Matches  275;  Conservative   29;  Mismatches   71;  Indels   91;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFLTKGPSKLN---- 77
              | | | :: |:| ||         :|      |    :  : : ||: |  |  :
Db       4414 LVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSY-TYYPDSVKGRFT 4472

Qy         78 -DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ- 135
               | ::: ||:      | : :|: ||:  | |  |:              | : :
Db       4473 ISRDNAKNSLY------LQMSSLRAEDTAVYYCAREE-------------NGNFYYFDY 4512

Qy        136 -GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||  |:|: |     |||   :|  |:  ||             : ::||
Db       4513 WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 4572

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |  | |    |:|       |||||
Db       4573 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 4626

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4627 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 4686

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4687 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 4746

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4747 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 4806

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db       4807 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 4852


RESULT 12
US-10-435-299-7
; Sequence 7, Application US/10435299
; Publication No. US20040052783A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Gingrich, Roger
;  APPLICANT:  Link, Brian
;  APPLICANT:  Tso, J. Yun
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
;  FILE REFERENCE: 05882-0176-CNUS04
;  CURRENT APPLICATION NUMBER: US/10/435,299
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 09/618,380
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: US 08/397,411
;  PRIOR FILING DATE: 1995-03-01
;  PRIOR APPLICATION NUMBER: US 07/859,583
;  PRIOR FILING DATE: 1992-03-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Complete heavy chain of Humanized 1D10 Ab
US-10-435-299-7

  Query Match             47.5%;  Score 1282.5;  DB 12;  Length 446;
  Best Local Similarity   59.8%;  Pred. No. 5.5e-78;
  Matches  274;  Conservative   25;  Mismatches   80;  Indels   79;  Gaps   10;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL- 86
              | |  :|: |||| |      :  ||   :  | |   |   : | :: |    || ::
Db         11 LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 70

Qy         87 --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
                 :    | : :|   |:  | |                   | :| : :   ||   :|
Db         71 KDTSKNQVSLKLNSLTAADTAVYYC----------------ARNDRYAMDYWGQGTLVT 113

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLEL 176
              : |     |||   :|  |:  ||             : ::||                |
Db        114 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 173

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                |: | |  | |    |:|       ||||||||||
Db        174 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP 227

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 287

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 347

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 407

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        408 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 445


RESULT 13
US-10-363-427-18
; Sequence 18, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
;  APPLICANT: MeDexGen Inc.
;  APPLICANT:  CHUNG, Yong Hoon
;  APPLICANT:  HAN, Ji Woong
;  APPLICANT:  LEE, Hye Ja
;  APPLICANT:  CHOI, Eun Yong
;  APPLICANT:  KIM, Jin Mi
;  APPLICANT:  YIM, Soo Bin
;  TITLE OF INVENTION: Concatametric Immunoadhesion
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/363,427
;  CURRENT FILING DATE:  2003-02-28
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 18
;   LENGTH: 617
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-363-427-18

  Query Match             47.5%;  Score 1282.5;  DB 14;  Length 617;
  Best Local Similarity   64.5%;  Pred. No. 8.3e-78;
  Matches  272;  Conservative   22;  Mismatches   63;  Indels   65;  Gaps   11;
```

```
Qy         35 DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL 94
Db        235 DDIKWEKTSDKKKIAQFRKEKE----------TFKEKDTYKLFK-----------NGTL 272

Qy         95 IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ----------SLTLT 142
Db        273 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-------IQERVSKPKISWTCINTTLT 325

Qy        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT--------CTVLQNQKKVE 194
Db        326 CEVMNGTDPELNL-------YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 375

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
Db        376 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 434

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
Db        435 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVCHQDWLNGKEYKCKVS 494

Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
Db        495 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 554

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
Db        555 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 614

Qy        430 PG 431
Db        615 PG 616
```

```
RESULT 14
US-10-363-427-22
; Sequence 22, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
;  APPLICANT: MeDexGen Inc.
;  APPLICANT:  CHUNG, Yong Hoon
;  APPLICANT:  HAN, Ji Woong
;  APPLICANT:  LEE, Hye Ja
;  APPLICANT:  CHOI, Eun Yong
;  APPLICANT:  KIM, Jin Mi
;  APPLICANT:  YIM, Soo Bin
;  TITLE OF INVENTION: Concatametric Immunoadhesion
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/363,427
;  CURRENT FILING DATE:  2003-02-28
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 22
;   LENGTH: 617
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-363-427-22

  Query Match             47.5%;  Score 1282.5;  DB 14;  Length 617;
  Best Local Similarity   64.5%;  Pred. No. 8.3e-78;
  Matches  272;  Conservative   22;  Mismatches   63;  Indels   65;  Gaps   11;

Qy         35 DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL 94
Db        235 DDIKWEKTSDKKKIAQFRKEKE----------TFKEKDTYKLFK-----------NGTL 272

Qy         95 IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ----------SLTLT 142
Db        273 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-------IQERVSKPKISWTCINTTLT 325

Qy        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT--------CTVLQNQKKVE 194
Db        326 CEVMNGTDPELNL-------YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 375

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
Db        376 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 434

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
Db        435 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVCHQDWLNGKEYKCKVS 494

Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
Db        495 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 554

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
Db        555 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 614

Qy        430 PG 431
Db        615 PG 616
```

```
RESULT 15
US-10-418-836-38
; Sequence 38, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
;  APPLICANT: Power, Scott D.
;  APPLICANT:  Wang, Huaming
;  APPLICANT:  Ward, Michael
;  TITLE OF INVENTION: Production of Functional Antibodies in
;  TITLE OF INVENTION:  Filamentous Fungi
;  FILE REFERENCE: GC741-2
;  CURRENT APPLICATION NUMBER: US/10/418,836
;  CURRENT FILING DATE:  2003-04-17
;  PRIOR APPLICATION NUMBER: US 60/373,889
;  PRIOR FILING DATE: 2002-04-18
;  PRIOR APPLICATION NUMBER: US 60/411,540
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: US 60/452,134
;  PRIOR FILING DATE: 2003-03-04
;  PRIOR APPLICATION NUMBER: US 60/411,537
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 972
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion protein
US-10-418-836-38

  Query Match             47.5%;  Score 1282.5;  DB 15;  Length 972;
  Best Local Similarity   59.8%;  Pred. No. 1.5e-77;
  Matches  274;  Conservative   25;  Mismatches   80;  Indels   79;  Gaps   10;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL- 86
Db        537 LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 596

Qy         87 --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
Db        597 KDTSKNQVSLKLNSLTAADTAVYYC----------------ARNDRYAMDYWGQGTLVT 639

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLEL 176
Db        640 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 699

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
Db        700 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP 753
```

```
Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 813

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 873

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 933

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        934 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 971
```

RESULT 16
US-10-418-836-39
; Sequence 39, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; TITLE OF INVENTION: Filamentous Fungi
; FILE REFERENCE: GC741-2
; CURRENT APPLICATION NUMBER: US/10/418,836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373,889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411,540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452,134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411,537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 975
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-10-418-836-39

Query Match 47.5%; Score 1282.5; DB 15; Length 975;
Best Local Similarity 59.8%; Pred. No. 1.5e-77;
Matches 274; Conservative 25; Mismatches 80; Indels 79; Gaps 10;

```
Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL- 86
              | |  :|: |||| |      :  ||   :  | |   |   : | :: |    || ::
Db        540 LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 599

Qy         87 --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
                 :    | : :|   |:  | |                 | :| : :   ||   :|
Db        600 KDTSKNQVSLKLNSLTAADTAVYYC----------------ARNDRYAMDYWGQGTLVT 642

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
              : |     |||   :|  |:  ||            : ::||            |
Db        643 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 702

Qy        177 QDSG----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||              |: | |  | |    |:|       ||||||||||
Db        703 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP 756

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 816

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 876

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 936

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        937 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 974
```

RESULT 17
US-10-404-724-23
; Sequence 23, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-23

Query Match 47.4%; Score 1281.5; DB 12; Length 465;
Best Local Similarity 57.7%; Pred. No. 6.8e-78;
Matches 284; Conservative 24; Mismatches 79; Indels 105; Gaps 13;

```
Qy         11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG 66
              || |  |   |  |   |  |    | |::|:::| ||      |     | :|    ||
Db          7 LLFLMAAAQSAQAQIQLVQSGPEVKKPGESVKISCKAS---GYTFTKYGMNWVKQAPGQG 63

Qy         67 -------SFLTKGPSKLNDRADSRRSLWDQGNFP-----------LIIKNLKIEDSDTYI 108
                    :  |: |:  :|          :| |             | | :|: ||: ||
Db         64 LKWMGWINTYTEEPTYGDD---------FKGRFTFTLDTSTSTAYLEISSLRSEDTATYF 114

Qy        109 CEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
              |              ||   :      ||   :|: |     |||   :|  |:  ||
Db        115 C-----------ARFGSAVD-----YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA 158

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||                || ||                 |: |
Db        159 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 218

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
              |  | |    |:|       ||||||||||      |||||||||||||||||||||||
Db        219 NV--NHKPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 272

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 332

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 392

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 452

Qy        420 HYTQKSLSLSPG 431
              ||||||||||||
Db        453 HYTQKSLSLSPG 464
```

```
RESULT 18
US-10-656-769-32
; Sequence 32, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
;  APPLICANT: Varnum, Brian
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Vezina, Chris
;  APPLICANT:  Wong, Lu Min
;  APPLICANT:  Qian, Xueming
;  TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
;  FILE REFERENCE: 01,1554
;  CURRENT APPLICATION NUMBER: US/10/656,769
;  CURRENT FILING DATE:  2003-09-05
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-769-32

  Query Match             47.4%;  Score 1280;  DB 16;  Length 467;
  Best Local Similarity   57.1%;  Pred. No. 8.6e-78;
  Matches  280;  Conservative   28;  Mismatches   78;  Indels  104;  Gaps   14;

Qy         16 LALLPAATQG---------NKVVLGKKGDTVELTCTASQKKSIQFHW---------KNSN 57
              ||||  |  ||         :   : | |:::::|  |   |  |||         |
Db          7 LALLLAVLQGVCAEVQLMQSGAEVKKPGESLKISCKGS-GYSFSFHWIAWVRQMPGKGLE 65

Qy         58 QIKILGNQGSFLTKGPS---KLNDRADSRRSL----WDQGNFPLIIKNLKIEDSDTYICE 110
              : |:    |    ||   ::   ||: |    |          :||  |:  | |
Db         66 WMGIIHPGASDTRYSPSFQGQVTISADNSNSATYLQW---------SSLKASDTAMYFCA 116

Qy        111 VEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---- 166
                 :: |:    :             ||   :|: |     |||   :|  |:  ||
Db        117 ---RQRELDYFDY-----------WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL 162

Qy        167 ---------KTLSVS-------------QLELQDSG-----------------TWTCTV 186
                      : ::||               || ||                    |: | |
Db        163 GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV 222

Qy        187 LQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRT 241
              | |    |:|       ||||||||||     |||||||||||||||||||||||||
Db        223 --NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT 276

Qy        242 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 336

Qy        302 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD 396

Qy        362 IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY 456

Qy        422 TQKSLSLSPG 431
              ||||||||||
Db        457 TQKSLSLSPG 466


RESULT 19
US-09-747-669-3
; Sequence 3, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:
;  APPLICANT: Dan, Michael D.
;  APPLICANT:  Saleh, Mansoor
;  TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
;  TITLE OF INVENTION:  4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
;  TITLE OF INVENTION:  ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
;  TITLE OF INVENTION:  AND DETECTION OF CANCERS
;  FILE REFERENCE: 316082001001
;  CURRENT APPLICATION NUMBER: US/09/747,669
;  CURRENT FILING DATE:  2002-04-08
;  PRIOR APPLICATION NUMBER: US 09/111,286
;  PRIOR FILING DATE: 1998-07-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-747-669-3

  Query Match             47.4%;  Score 1280;  DB 9;  Length 476;
  Best Local Similarity   56.9%;  Pred. No. 8.8e-78;
  Matches  280;  Conservative   27;  Mismatches   91;  Indels   94;  Gaps   12;

Qy         11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFH---------- 52
              :| |  |   | :|   |  |    | | :|:::| ||       |
Db          7 VLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLNWVRQAPGQGLEW 66

Qy         53 --WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICE 110
                | | |  |          |   |    |     |:   :  : : :  |: ||:  | |
Db         67 MGWMNPNSGK---------TGYAQKFQGRVTMTRNTSIRTAY-MELSGLRSEDTAVYFCA 116

Qy        111 VEDQKEEVQLL--VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
                    |:  :   :|:         : ||  |:|: |      |||   :|  |:  ||
Db        117 RNADNVEMAAIYHYYGMD-------VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA 169

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||               || ||                    |: |
Db        170 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 229

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
              |  | |    |:|       ||||||||||     |||||||||||||||||||||||
Db        230 NV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 283

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 343

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 403

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 463

Qy        420 HYTQKSLSLSPG 431
              ||||||||||||
Db        464 HYTQKSLSLSPG 475


RESULT 20
US-10-290-703-3
; Sequence 3, Application US/10290703
; Publication No. US20030118593A1
; GENERAL INFORMATION:
;  APPLICANT: Dan, Michael D.
;  APPLICANT:  Saleh, Mansoor
;  TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
;  TITLE OF INVENTION:  4B5, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
;  TITLE OF INVENTION:  ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
;  TITLE OF INVENTION:  AND DETECTION OF CANCERS
;  FILE REFERENCE: 316082001002
;  CURRENT APPLICATION NUMBER: US/10/290,703
;  CURRENT FILING DATE:  2002-11-08
;  PRIOR APPLICATION NUMBER: US 09/747,669
```

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;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: US 09/111,286
;  PRIOR FILING DATE: 1998-07-07.
;  PRIOR APPLICATION NUMBER: US 60/051,945
;  PRIOR FILING DATE: 1997-07-08
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-290-703-3

  Query Match             47.4%;  Score 1280;  DB 14;  Length 476;
  Best Local Similarity   56.9%;  Pred. No. 8.8e-78;
  Matches  280;  Conservative   27;  Mismatches   91;  Indels   94;  Gaps   12;

Qy         11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFH---------- 52
                :| |  |   | :|   |  |    | | :|:::| ||     |
Db          7 VLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLNWVRQAPGQGLEW 66

Qy         53 --WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICE 110
                 | | |  |         |    |   |     |:   :  : : :  |: ||:  | |
Db         67 MGWMNPNSGK---------TGYAQKFQGRVTMTRNTSIRTAY-MELSGLRSEDTAVYFCA 116

Qy        111 VEDQKEEVQLL--VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
                      |:  :   :|:        : ||  |:|: |      |||   :|  |:  ||
Db        117 RNADNVEMAAIYHYYGMD-------VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA 169

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||              || ||                    |: |
Db        170 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 229

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
                |  | |    |:|       ||||||||||     ||||||||||||||||||||||
Db        230 NV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 283

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 343

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 403

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 463

Qy        420 HYTQKSLSLSPG 431
              ||||||||||||
Db        464 HYTQKSLSLSPG 475


RESULT 21
US-10-378-567-2
; Sequence 2, Application US/10378567
; Publication No. US20040006208A1
; GENERAL INFORMATION:
;  APPLICANT: KARPUSAS, MICHAEL
;  APPLICANT:  HSU, YEN-MING
;  APPLICANT:  TAYLOR, FREDERICK R.
;  APPLICANT:  ZHENG, ZHONGLI
;  TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND
;  TITLE OF INVENTION:  CD154, AND USE THEREOF IN DRUG DESIGN
;  FILE REFERENCE: A096CON1
;  CURRENT APPLICATION NUMBER: US/10/378,567
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/27352
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: 60/276,452
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/229,933
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: humanized 5c8 heavy chain amino acid
US-10-378-567-2

  Query Match             47.4%;  Score 1279.5;  DB 15;  Length 448;
  Best Local Similarity   58.9%;  Pred. No. 8.8e-78;
  Matches  275;  Conservative   31;  Mismatches   74;  Indels   87;  Gaps   13;

Qy         25 GNKVVLGKKGDTVELTCTASQK--KSIQFHWKNSNQIKILGNQG-SFL-----TKGPSKL 76
                | :||  | | :|:|:| ||      |   :|     :|    ||  ::     : | :
Db          8 GAEVV--KPGASVKLSCKASGYIFTSYYMYW-----VKQAPGQGLEWIGEINPSNGDTNF 60

Qy         77 NDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
               |::  |: :|          : : :|: ||:  | |   | : ::
Db         61 NEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTRSDGRNDMD-------------- 106

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------- 172
                 ||   :|: |      |||   :|  |:  ||              : ::||
Db        107 SWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 166

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                    || ||                   |: | |  | |     |:|        ||||
Db        167 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKS 220

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 280

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 340

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 400

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 447


RESULT 22
US-10-207-655-344
; Sequence 344, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 344
;   LENGTH: 492
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion polypeptide
US-10-207-655-344

  Query Match             47.3%;  Score 1279;  DB 14;  Length 492;
```

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  Best Local Similarity   55.8%;  Pred. No. 1.1e-77;
  Matches  279;  Conservative   33;  Mismatches   92;  Indels   96;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |:|||      :||         ||     :    |: | :|| ||    |  : ::  :
Db         19 MSRGVD-----IVL--------TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS--- 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE--------- 110
                |          |||      :| |     | :: | |   :: ||: || |:
Db         63 --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120

Qy        111 -----VEDQK-------------EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                  :| ::              :|||   |       |  |   ||| |:     :|
Db        121 GSGTKLEIKRGGGGSGGGGSGGGGSQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD 177

Qy        152 SVQ-CRSPRGKNIQ--------GGKT--------------------LSVSQLELQDSGT 181
               |   | | || ::        ||                     | :: |:  |:
Db        178 GVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM 237

Qy        182 WTCTVLQNQKKVEPK-----IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPK 231
              : |       :: |      : :       ||||||||||     ||||||||||||||
Db        238 YYCA------RIHFDYWGQGVMVTVSSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 291

Qy        232 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 351

Qy        292 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 411

Qy        352 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 471

Qy        412 VMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||
Db        472 VMHEALHNHYTQKSLSLSPG 491


RESULT 23
US-10-108-260A-4292
; Sequence 4292, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4292
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-4292

  Query Match             47.3%;  Score 1277.5;  DB 15;  Length 470;
  Best Local Similarity   58.8%;  Pred. No. 1.3e-77;
  Matches  281;  Conservative   31;  Mismatches   77;  Indels   89;  Gaps   14;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKN----------SNQIKIL 62
              |: |: : |:     : | | :|:::| ||     |  | |              : | ||
Db         20 QVQLVQSGTE-----VKKPGSSVKVSCKASGGSFSSYVFTWVRQAPGEGLEWMGSIIPIL 74

Qy         63 GNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              | : ::  |   ::   ||   |:       : :  | |||:  | | :          ||
Db         75 G-RPNYAQKFQDRVTISADESSSI-----VYMDLDRLTIEDTAIYFCAI--------LLE 120

Qy        123 FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTL 169
                : |  | |  ||  :|::  |  |  |||   :|  |:  ||             : :
Db        121 HEVRALFD-HWGQGTLVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177

Qy        170 SVS-------------QLELQDSG-----------------TWTCTVLQNQKKVEFKID 198
              :||                 || ||                 |: | |  | ||    |:|
Db        178 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD 235

Qy        199 IVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 253
                      ||||||||||     ||||||||||||||||||||||||||||||||||||
Db        236 ----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 291

Qy        254 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 351

Qy        314 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 373
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 PAPIEKTISKAKGQPREPQVYALPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 411

Qy        374 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469


RESULT 24
US-10-207-655-345
; Sequence 345, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
;   LENGTH: 543
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion polypeptide
US-10-207-655-345

  Query Match             47.3%;  Score 1277;  DB 14;  Length 543;
  Best Local Similarity   55.8%;  Pred. No. 1.7e-77;
  Matches  279;  Conservative   33;  Mismatches   92;  Indels   96;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |:|||      :||         ||     :    |: | :|| ||    |  : ::  :
Db         19 MSRGVD-----IVL--------TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS--- 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE--------- 110
                |          |||      :| |     | :: | |   :: ||: || |:
Db         63 --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120

Qy        111 -----VEDQK-------------EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                  :| ::              :|||   |       |  |   ||| |:     :|
Db        121 GSGTKLEIKRGGGGSGGGGSGGGGSQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD 177

Qy        152 SVQ-CRSPRGKNIQ--------GGKT--------------------LSVSQLELQDSGT 181
               |   | | || ::        ||                     | :: |:  |:
Db        178 GVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM 237

Qy        182 WTCTVLQNQKKVEPK-----IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPK 231
              : |       :: |      : :       ||||||||||     ||||||||||||||
Db        238 YYCA------RIHFDYWGQGVMVTVSSDLEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 291

Qy        232 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 351

Qy        292 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        352 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 411

Qy        352 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 471

Qy        412 VMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||
Db        472 VMHEALHNHYTQKSLSLSPG 491


RESULT 25
US-09-740-002-25
; Sequence 25, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/09/740,002
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-740-002-25

  Query Match             47.2%;  Score 1276.5;  DB 9;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 1.5e-77;
  Matches  281;  Conservative   27;  Mismatches   87;  Indels   97;  Gaps   12;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----------------QKKSIQFHWK 54
              |: |    |      | :  |: |  :|: |||| |                |       |
Db         10 LVAVATRVLSQVQLQESGPVVVKPTETLTLTCTVSGFSLSNPRMGVTWIRQPPGKALEW- 68

Qy         55 NSNQIKILGN-----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC 109
                 |||      : ||      |:|     |: ||         | : |:    |: || |
Db         69 -------LGNIFSSDEKSFSPSLKSRLTTSQDTSRS-----QVVLSLTNVDPVDTATYYC 116

Qy        110 EVEDQKEEVQLLVFGLTANSDTHL-LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
                  :: :: : |    :|    ||   :|: |      |||   :|  |:  ||
Db        117 --------ARVGLYDINAYYLYYLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA 168

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||                || ||                    |: |
Db        169 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 228

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
                |  | |    |:|        ||||||||||     |||||||||||||||||||||||
Db        229 NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 282

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        283 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQEWL 342

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 402

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 462

Qy        420 HYTQKSLSLSPG 431
              ||||||||||||
Db        463 HYTQKSLSLSPG 474


RESULT 26
US-10-325-698-25
; Sequence 25, Application US/10325698
; Publication No. US20040076631A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/10/325,698
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/740,002
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-325-698-25

  Query Match             47.2%;  Score 1276.5;  DB 16;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 1.5e-77;
  Matches  281;  Conservative   27;  Mismatches   87;  Indels   97;  Gaps   12;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----------------QKKSIQFHWK 54
              |: |    |      | :  |: |  :|: |||| |                |       |
Db         10 LVAVATRVLSQVQLQESGPVVVKPTETLTLTCTVSGFSLSNPRMGVTWIRQPPGKALEW- 68

Qy         55 NSNQIKILGN-----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC 109
                 |||      : ||      |:|     |: ||         | : |:    |: || |
Db         69 -------LGNIFSSDEKSFSPSLKSRLTTSQDTSRS-----QVVLSLTNVDPVDTATYYC 116

Qy        110 EVEDQKEEVQLLVFGLTANSDTHL-LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
                  :: :: : |    :|    ||   :|: |      |||   :|  |:  ||
Db        117 --------ARVGLYDINAYYLYYLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA 168

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||                || ||                    |: |
Db        169 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 228

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
                |  | |    |:|        ||||||||||     |||||||||||||||||||||||
Db        229 NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 282

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        283 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQEWL 342

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 402

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 462

Qy        420 HYTQKSLSLSPG 431
              ||||||||||||
Db        463 HYTQKSLSLSPG 474


RESULT 27
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US-10-138-727A-41
; Sequence 41, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin-Ming
;  APPLICANT:  Qian, Susan
;  TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
;  FILE REFERENCE: LEX-019
;  CURRENT APPLICATION NUMBER: US/10/138,727A
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US 60/288,564
;  PRIOR FILING DATE: 2001-05-03
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
;   LENGTH: 579
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: heavy chain-IL2
US-10-138-727A-41

  Query Match             47.2%;  Score 1275.5;  DB 14;  Length 579;
  Best Local Similarity   57.7%;  Pred. No. 2.3e-77;
  Matches  281;  Conservative   29;  Mismatches   70;  Indels  107;  Gaps   14;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLW 87
              | |:||:::| ||      :  :|      | |   |  :  |  |:  :|
Db         13 KPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTYADD--------- 63

Qy         88 DQGNFP-----------LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              :| |           | | ||: ||: || |       |: :  |       :  ||
Db         64 FKGRFAFSLETSTSTAFLQINNLRSEDTATYFC--------VRFISKG------DYWGQG 109

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |:|::  |  |  |||   :|  |:  ||             : ::||
Db        110 TSVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 167

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                  || ||                 |: | |  | |    |:|       |||||||
Db        168 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK 221

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 281

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 341

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        342 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 401

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----------LQLD 435
              |||||||||||||||||||||||||||||||||||||||||||||           |||:
Db        402 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLE 461

Qy        436 ETCAEAQ 442
                : |
Db        462 HLLLDLQ 468


RESULT 28
US-10-334-235-38
; Sequence 38, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: peptide of 5T4Sab1
US-10-334-235-38

  Query Match             47.2%;  Score 1275;  DB 16;  Length 600;
  Best Local Similarity   59.4%;  Pred. No. 2.6e-77;
  Matches  277;  Conservative   18;  Mismatches   81;  Indels   90;  Gaps   11;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              ||    :|   || | :|| |||  |   |                 : |: |     |
Db        162 TQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKP----------GQSPTLLISYTSS 210

Qy         83 R-RSLWDQ-------GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL 134
              |   : |:        :|   |  |: ||   | |: :               ||
Db        211 RYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQD-------------YNSPPTFG 256

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
              |  | :   |  .|  |||   :|  |:  ||             : ::||
Db        257 GGTKLEIKRASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 314

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                    || ||                 |: | |  | |    |:|       |||||
Db        315 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 368

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 428

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 488

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 548

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        549 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 594


RESULT 29
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
;  APPLICANT: Neben, Steven
;  APPLICANT:  Takeuchi, Toshihiko
;  APPLICANT:  Tomkinson, Adrian
;  TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
;  TITLE OF INVENTION:  Treatment Of Asthma
;  FILE REFERENCE: 7430*163
;  CURRENT APPLICATION NUMBER: US/10/320,231A
```

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;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/342,174
;  PRIOR FILING DATE: 2001-12-17
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

  Query Match             47.2%;  Score 1274.5;  DB 14;  Length 445;
  Best Local Similarity   59.2%;  Pred. No. 1.9e-77;
  Matches  277;  Conservative   27;  Mismatches   67;  Indels   97;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFL----TKG 72
              | : | :: |:| ||             |       | ::    | |: ||       ||
Db          8 LVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA----ISGSGGSTYYADSVKG 63

Qy         73 PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH 132
                 :: | :|: :|: | |       :|: ||:  | |   |              |: |
Db         64 RFTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCARRD-----------FFAHFD-- 103

Qy        133 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------- 172
               : ||   :|: |     |||   :|  |:  ||              : ::||
Db        104 -VWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 162

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                   || ||                    |: | |  | |    |:|       |||
Db        163 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 216

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 276

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 336

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 396

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 444


RESULT 30
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, G. et al.
;  TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1211
;  CURRENT APPLICATION NUMBER: US/10/150,475A
;  CURRENT FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/307,451
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Humanised
;   OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

  Query Match             47.1%;  Score 1273.5;  DB 14;  Length 444;
  Best Local Similarity   59.3%;  Pred. No. 2.2e-77;
  Matches  275;  Conservative   27;  Mismatches   69;  Indels   93;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFL-----TKGPSKL 76
              | | | :: |:| ||      |    |       |    :  : : ||:       ||   :
Db         11 LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: ||: | |      :|: ||:  | |  :            ||        |
Db         71 S-RDNAKNSLYLQMN------SLRAEDTAVYYCARQ-----------GLD-------YWG 105

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              :   :|: |      |||   :|  |:  ||              : ::||
Db        106 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 165

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                    |: | |  | |    |:|       |||||||
Db        166 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 219

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 279

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 339

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 399

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        400 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443


RESULT 31
US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Gunther
;  APPLICANT:  Baumann, Michael
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and methods for treating cancer using
;  TITLE OF INVENTION:  cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1414
;  CURRENT APPLICATION NUMBER: US/10/704,522
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: US 60/429,516
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: EP 02024881
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6

  Query Match             47.1%;  Score 1273.5;  DB 16;  Length 444;
  Best Local Similarity   59.3%;  Pred. No. 2.2e-77;
  Matches  275;  Conservative   27;  Mismatches   69;  Indels   93;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFL-----TKGPSKL 76
              | | | :: |:| ||      |    |       |    :  : : ||:       ||   :
Db         11 LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
```

```
           : | ::: ||: | |      :|: ||:  | |  :          ||          |
Db         71 S-RDNAKNSLYLQMN------SLRAEDTAVYYCARQ-----------GLD-------YWG 105

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              :   :|: |      |||   :|  |:  ||             : ::||
Db        106 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 165

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |     |:|       |||||||
Db        166 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 219

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 279

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 339

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 399

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        400 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443
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RESULT 32
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6

Query Match 47.1%; Score 1273.5; DB 16; Length 444;
Best Local Similarity 59.3%; Pred. No. 2.2e-77;
Matches 275; Conservative 27; Mismatches 69; Indels 93; Gaps 13;

```
Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFL-----TKGPSKL 76
              | | | :: |:| ||      |    |       |    :  : : ||:       ||   :
Db         11 LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: ||: | |      :|: ||:  | |  :          ||          |
Db         71 S-RDNAKNSLYLQMN------SLRAEDTAVYYCARQ-----------GLD-------YWG 105

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              :   :|: |      |||   :|  |:  ||             : ::||
Db        106 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 165

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |     |:|       |||||||
Db        166 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 219

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 279

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 339

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 399

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        400 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443
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RESULT 33
US-09-740-002-27
; Sequence 27, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-27

Query Match 47.1%; Score 1273.5; DB 9; Length 475;
Best Local Similarity 57.1%; Pred. No. 2.4e-77;
Matches 276; Conservative 29; Mismatches 99; Indels 79; Gaps 11;

```
Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKIL--- 62
              |: |    |     | :   | |   |: |||| |      : :  :|      | |
Db         10 LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL 69

Qy         63 ----GNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE 117
                    :  :| :    ::|:   |: ::        | : |:   |: || |      :
Db         70 ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS 124

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG----------- 166
                 :|         |   ||   :|: |      |||   :|  |:  ||
Db        125 DSFYLF-------YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 177

Qy        167 --KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKV 193
                 : ::||             || ||                  |: | |  | ||
Db        178 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 235

Qy        194 EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
                |:|       ||||||||||      |||||||||||||||||||||||||||||
Db        236 NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 291

Qy        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 351
```

```
Qy        309 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 411

Qy        369 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 471

Qy        429 SPG 431
              |||
Db        472 SPG 474


RESULT 34
US-10-325-698-27
; Sequence 27, Application US/10325698
; Publication No. US20040076631A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/10/325,698
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/740,002
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-325-698-27

  Query Match             47.1%;  Score 1273.5;  DB 16;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 2.4e-77;
  Matches  276;  Conservative   29;  Mismatches   99;  Indels   79;  Gaps   11;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKIL--- 62
              |: |    |     | :   | |   |: |||| |      : :  :|       | |
Db         10 LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL 69

Qy         63 ----GNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE 117
                  :  :| :    ::|:   |: ::         | : |:   |: || |      :
Db         70 ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS 124

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                :|          |  ||   :|: |     |||   :|  |:  ||
Db        125 DSFYLF-------YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 177

Qy        167 --KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKV 193
                : ::||             || ||                  |: | |  | |
Db        178 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 235

Qy        194 EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
                |:|       ||||||||||     ||||||||||||||||||||||||||||||||
Db        236 NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 291

Qy        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 351

Qy        309 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 411

Qy        369 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 471

Qy        429 SPG 431
              |||
Db        472 SPG 474


RESULT 35
US-10-683-255-6
; Sequence 6, Application US/10683255
; Publication No. US20040063910A1
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh, William M.
;  APPLICANT:  Ballinger, Marcus
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: PP01474.101
;  CURRENT APPLICATION NUMBER: US/10/683,255
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: 09/499,846
;  PRIOR FILING DATE: 2000-02-07
;  PRIOR APPLICATION NUMBER: 60/119,002
;  PRIOR FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-683-255-6

  Query Match             47.1%;  Score 1273.5;  DB 12;  Length 497;
  Best Local Similarity   57.5%;  Pred. No. 2.5e-77;
  Matches  276;  Conservative   30;  Mismatches   83;  Indels   91;  Gaps   12;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
              :|  :|||              ||:  | :|    :    | ||  : |    | | :  :
Db         45 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 92

Qy         70 TKG-------PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |         ||             |:||:  |::|     : ||  :| ::      :|
Db         93 TWSIIMDSVVPS------------DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 139

Qy        123 FGLTANSDTHLLQGQSLTLTLESPP------------GSS------PSVQCRSPRGKNI 163
               || ||    |          : | |               ||       | ||     | |
Db        140 AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT 199

Qy        164 --QGGKTLSVSQLELQDSGTWTC--------------TVLQNQKKVEFKIDIVPCP--- 203
                :  : | :  :  :|:| :||              |||:   :| :  ::  |
Db        200 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 256

Qy        204 -------APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                    ||||||||||     ||||||||||||||||||||||||||||||||||||||
Db        257 EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 316

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 376

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 436

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 496


RESULT 36
US-10-683-255-4
; Sequence 4, Application US/10683255
; Publication No. US20040063910A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh, William M.
;  APPLICANT:  Ballinger, Marcus
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: PP01474.101
;  CURRENT APPLICATION NUMBER: US/10/683,255
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: 09/499,846
;  PRIOR FILING DATE: 2000-02-07
;  PRIOR APPLICATION NUMBER: 60/119,002
;  PRIOR FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 525
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-683-255-4

  Query Match             47.1%;  Score 1273.5;  DB 12;  Length 525;
  Best Local Similarity   57.5%;  Pred. No. 2.7e-77;
  Matches  276;  Conservative   30;  Mismatches   83;  Indels   91;  Gaps   12;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
              :|  :|||              ||:  | :|   :    | ||  : |     | | :  :
Db         73 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120

Qy         70 TKG-------PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |          ||              |:||:  |::|     : ||  :| ::     :|
Db        121 TWSIIMDSVVPS------------DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 167

Qy        123 FGLTANSDTHLLQGQSLTLTLESPP------------GSS------PSVQCRSPRGKNI 163
               || ||    |          : | |              ||       | ||     | |
Db        168 AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT 227

Qy        164 --QGGKTLSVSQLELQDSGTWTC---------------TVLQNQKKVEFKIDIVPCP--- 203
                :  : | :  :  :|:| :||               |||:    :| :  ::  |
Db        228 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 284

Qy        204 -------APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                    ||||||||||     |||||||||||||||||||||||||||||||||||||||
Db        285 EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 344

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 404

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 464

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 524


RESULT 37
US-10-683-255-2
; Sequence 2, Application US/10683255
; Publication No. US20040063910A1
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh, William M.
;  APPLICANT:  Ballinger, Marcus
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: PP01474.101
;  CURRENT APPLICATION NUMBER: US/10/683,255
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: 09/499,846
;  PRIOR FILING DATE: 2000-02-07
;  PRIOR APPLICATION NUMBER: 60/119,002
;  PRIOR FILING DATE: 1999-02-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 622
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-683-255-2

  Query Match             47.1%;  Score 1273.5;  DB 12;  Length 622;
  Best Local Similarity   57.0%;  Pred. No. 3.4e-77;
  Matches  276;  Conservative   31;  Mismatches   86;  Indels   91;  Gaps   12;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIKILGNQGSFLTKGP 73
              :|  :|||              ||:  | :|   :    | ||  : |     | :
Db        162 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKV--- 206

Qy         74 SKLNDRADSRRSLW----------DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF 123
                        | : |          |:||:  |::|     : ||  :| ::     :|
Db        207 ---------RYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQA 257

Qy        124 GLTANSDTHLLQGQSLTLTLESPP-------------GSS------PSVQCRSPRGKNI- 163
              || ||    |          : | |              ||       | ||     | |
Db        258 GLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTT 317

Qy        164 -QGGKTLSVSQLELQDSGTWTC---------------TVLQNQKK----------VEFKI 197
               :  : | :  :  :|:| :||               |||:  ::          :| :
Db        318 DKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLESRG 377

Qy        198 DIVP----CPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
               :|     |   ||||||||||     |||||||||||||||||||||||||||||||
Db        378 GLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 437

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 497

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 557

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 617

Qy        428 LSPG 431
              ||||
Db        618 LSPG 621


RESULT 38
US-10-108-260A-4282
; Sequence 4282, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4282
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-4282

  Query Match             47.1%;  Score 1272.5;  DB 15;  Length 474;
  Best Local Similarity   57.5%;  Pred. No. 2.8e-77;
  Matches  280;  Conservative   28;  Mismatches   84;  Indels   95;  Gaps   13;

Qy         16 LALLPAATQGNKVV-----LGKKGDTVELTCTASQKKSIQF-----HWKNSNQIKILGNQ 65
              ||: | |    :::     : | | :|:::| ||      |      |      : |
```

```
Db         11 LAVAPGANSQAQLLQSGPEVRKPGASVKVSCKAS---GFDFTRDFLQWVRQAPGQGLEWM 67

Qy         66 GSFLTKGPSKL----------NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC--EVED 113

Db         68 GFIDPSGGSTLYAQNFQGRVTMTRERSTTTVY------MELSSLKSEDTATYFCCGSVN- 120

Qy        114 QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------- 166

Db        121 --------IVSTTSGGDPCDLWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL 172

Qy        167 ------KTLSVS-------------QLELQDSG-----------------TWTCTVLQN 189

Db        173 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--N 230

Qy        190 QKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV 244

Db        231 HKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV 286

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304

Db        287 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 346

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364

Db        347 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 406

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424

Db        407 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 466

Qy        425 SLSLSPG 431

Db        467 SLSLSPG 473
```

```
RESULT 39
US-10-660-128-12
; Sequence 12, Application US/10660128
; Publication No. US20040120947A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Chuntharapai, Anan
;  APPLICANT:  Dodge, Kelly
;  APPLICANT:  Kim, Kyung Jin
;  TITLE OF INVENTION: DR4 Antibodies and Uses Thereof
;  FILE REFERENCE: P1245R1P2B
;  CURRENT APPLICATION NUMBER: US/10/660,128
;  CURRENT FILING DATE:  2003-09-11
;  PRIOR APPLICATION NUMBER: US/09/584,166
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: US 09/322,875
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: US 09/237,299
;  PRIOR FILING DATE: 1999-01-25
;  PRIOR APPLICATION NUMBER: US 60/072,481
;  PRIOR FILING DATE: 1998-01-26
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 12
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
;   FEATURE:
;   NAME/KEY: Misc_feature
;   LOCATION: 20
;   OTHER INFORMATION: Xaa may be glutamine or glutamic acid
US-10-660-128-12

  Query Match           47.1%;  Score 1272;  DB 16;  Length 476;
  Best Local Similarity   60.4%;  Pred. No. 3e-77;
  Matches  273;  Conservative   29;  Mismatches   82;  Indels   68;  Gaps   12;
```

```
Qy         36 TVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNF 92

Db         36 SLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAVGSTNYNSALMSRLSISKDNSKS 95

Qy         93 PLIIK--NLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLTLESPPG 148

Db         96 QVFLKMNSLQTDDTAMYYCAREGEFD-----YYGSSLLS-YHSMNFWGQGTSVTVSSAKT 149

Qy        149 SSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG-- 180

Db        150 TGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 209

Qy        181 ----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL 219

Db        210 SLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPEL 263

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279

Db        264 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 323

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339

Db        324 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399

Db        384 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 443

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431

Db        444 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
```

```
RESULT 40
US-10-159-006-18
; Sequence 18, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT:  Garin-Chesa, Pilar
;  APPLICANT:  Bamberger, Uwe
;  APPLICANT:  Leger, Olivier
;  APPLICANT:  Saldanha, Jose W.
;  APPLICANT:  Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAPa-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890002
;  CURRENT APPLICATION NUMBER: US/10/159,006
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: US 09/301,593
;  PRIOR FILING DATE: 1999-04-29
;  PRIOR APPLICATION NUMBER: EP 98107925.4
;  PRIOR FILING DATE: 1998-04-30
;  PRIOR APPLICATION NUMBER: US 60/086,049
;  PRIOR FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-159-006-18

  Query Match           47.1%;  Score 1271.5;  DB 14;  Length 453;
  Best Local Similarity   59.0%;  Pred. No. 3.1e-77;
  Matches  271;  Conservative   31;  Mismatches   84;  Indels   73;  Gaps   12;
```

```
Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL 86

Db         10 LVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLEWIGGINPNNGIPNYNQKFKGRATL 69

Qy         87 W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141

Db         70 TVGKSSSTAYMELRSLTSEDSAVYFC-------ARRRIAYGY---DEGHAMDYWGQGTSV 119
```

```
Qy        142 TLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLE 175
              |: |     |||   :|  |:  ||             : ::||
Db        120 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC- 216
              || ||                 |: | |  | |    |:|       ||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP 233

Qy        217 ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 293

Qy        273 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 353

Qy        333 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 392
              ||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 413

Qy        393 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        414 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 452
```

RESULT 41
US-10-404-724-25
; Sequence 25, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-25

Query Match 47.1%; Score 1271.5; DB 12; Length 465;
Best Local Similarity 57.2%; Pred. No. 3.2e-77;
Matches 283; Conservative 23; Mismatches 78; Indels 111; Gaps 14;

```
Qy         11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG 66
              || |   |  |  |  |  |     | |::|:::| ||       |      | ::    ||
Db          7 LLFLMAAAQSAQAQIQLVQSGAEVKKPGESVKISCKAS---GYTFTKYGMNWVRQAPGQG 63

Qy         67 -------SFLTKGPS---KLNDRADSRRSLWDQGNFP-----------LIIKNLKIEDSD 105
                    :  |: |:   |              || |           | | :|: ||:
Db         64 LEWMGWINTYTEEPTYGQKF-----------QGRFTFTLDTSTSTAYLEISSLRSEDTA 111

Qy        106 TYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQG 165
               | |             ||   :       ||   :|: |     |||   :|  |:  |
Db        112 VYFC-----------ARFGSAVD-----YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG 155

Qy        166 G-------------KTLSVS-------------QLELQDSG-----------------T 181
              |             : ::||               || ||                 |
Db        156 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT 215

Qy        182 WTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTL 236
              : | |  | |    |:|       ||||||||||     ||||||||||||||||||||
Db        216 YICNV--NHKPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL 269

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        270 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 329

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 389

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 449

Qy        417 LHNHYTQKSLSLSPG 431
              |||||||||||||||
Db        450 LHNHYTQKSLSLSPG 464
```

RESULT 42
US-10-207-655-15
; Sequence 15, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MOUSE-HUMAN HYBRID FUSION PROTEIN
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(265)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV: 2H7
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (266)..(499)
; OTHER INFORMATION: HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC
US-10-207-655-15

Query Match 47.1%; Score 1271.5; DB 14; Length 499;
Best Local Similarity 56.6%; Pred. No. 3.5e-77;
Matches 275; Conservative 27; Mismatches 93; Indels 91; Gaps 12;

```
Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||          |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || |   |:          ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR----------------SPR------ 159
                   :|  :| | |  |       ||:|  : |:                   :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                         :  :|  ||:|            | |  :||  : |  :       :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
              |:      |     ||||||||||      ||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 312

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 432

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 492

Qy        426 LSLSPG 431
              ||||||
Db        493 LSLSPG 498


RESULT 43
US-10-207-655-148
; Sequence 148, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 148
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Mouse-Human hybrid fusion protein
US-10-207-655-148

  Query Match             47.1%;  Score 1271.5;  DB 14;  Length 499;
  Best Local Similarity   56.6%;  Pred. No. 3.5e-77;
  Matches  275;  Conservative   27;  Mismatches   93;  Indels   91;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||        |:          || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKGGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:                 :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :        :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
               |:      |     ||||||||||     ||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 312

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 432

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 492

Qy        426 LSLSPG 431
              ||||||
Db        493 LSLSPG 498


RESULT 44
US-10-053-530-15
; Sequence 15, Application US/10053530
; Publication No. US20030133939A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey
;  APPLICANT:  Hayden-Ledbetter, Martha
;  TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
;  FILE REFERENCE: 390069.401
;  CURRENT APPLICATION NUMBER: US/10/053,530
;  CURRENT FILING DATE:  2002-01-17
;  PRIOR APPLICATION NUMBER: US 09/765,208
;  PRIOR FILING DATE: 2001-01-17
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MOUSE-HUMAN HYBRID FUSION PROTEIN
;   NAME/KEY: SITE
;   LOCATION: (1)..(265)
;   OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV:  2H7
;   NAME/KEY: DOMAIN
;   LOCATION: (266)..(499)
;   OTHER INFORMATION: HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC
US-10-053-530-15

  Query Match             47.1%;  Score 1271.5;  DB 14;  Length 499;
  Best Local Similarity   56.6%;  Pred. No. 3.5e-77;
  Matches  275;  Conservative   27;  Mismatches   93;  Indels   91;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||        |:          || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:                 :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :        :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
               |:      |     ||||||||||     ||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 312

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 432

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 492

Qy        426 LSLSPG 431
              ||||||
Db        493 LSLSPG 498


RESULT 45
US-09-948-429B-12
```

```
; Sequence 12, Application US/09948429B
; Patent No. US20020177689A1
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/948,429B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/383,916
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/487,550
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-948-429B-12

  Query Match            47.0%;  Score 1271;  DB 9;  Length 476;
  Best Local Similarity  59.8%;  Pred. No. 3.5e-77;
  Matches  274;  Conservative   29;  Mismatches   87;  Indels   68;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |       : |     | |   |||  : | :  |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                :     :  | | : ::   |:  | | | |:   |  :|:     ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
              : |     |||   :|  |:  ||             : ::||               |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                 |: | |  | |    |:|       ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 46
US-09-758-173-12
; Sequence 12, Application US/09758173
; Publication No. US20010024648A1
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/758,173
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/383,916
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/487,550
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-758-173-12

  Query Match            47.0%;  Score 1271;  DB 12;  Length 476;
  Best Local Similarity  59.8%;  Pred. No. 3.5e-77;
  Matches  274;  Conservative   29;  Mismatches   87;  Indels   68;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |       : |     | |   |||  : | :  |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                :     :  | | : ::   |:  | | | |:   |  :|:     ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
              : |     |||   :|  |:  ||             : ::||               |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
```

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                | ||                  |: | |  | |    |:|      ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
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RESULT 47
US-10-124-905-12
; Sequence 12, Application US/10124905
; Publication No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-12

Query Match 47.0%; Score 1271; DB 13; Length 476;
Best Local Similarity 59.8%; Pred. No. 3.5e-77;
Matches 274; Conservative 29; Mismatches 87; Indels 68; Gaps 11;

```
Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
               | |  :|: |||  |        : |      | |   |||  : | :  |    |: :

Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                  :    : | | : ::   |: | | | |:   |  :|:     ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLEL 176
                : |     |||   :|  |:  ||             : ::||               |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
                | ||                 |: | |  | |    |:|      ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
```

RESULT 48
US-10-124-807-12
; Sequence 12, Application US/10124807
; Publication No. US20030166207A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids

```
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-124-807-12

  Query Match             47.0%;  Score 1271;  DB 14;  Length 476;
  Best Local Similarity   59.8%;  Pred. No. 3.5e-77;
  Matches  274;  Conservative   29;  Mismatches   87;  Indels   68;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |         : |      | |   ||| : | : |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
              :    :  | | : ::   |:  | | | |:   | :|:    ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
              : |     |||   :|  |:  ||             : ::||                |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                   |: | |  | |    |:|       ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 49
US-10-291-532-12
; Sequence 12, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
;  APPLICANT: HARIHARAN, KANDASAMY
;  APPLICANT:  HANNA, NABIL
;  TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
;  TITLE OF INVENTION:  MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
;  TITLE OF INVENTION:  COMBINATION WITH OTHER THERAPIES
;  FILE REFERENCE: 037003/291872
;  CURRENT APPLICATION NUMBER: US/10/291,532
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: 60/331,187
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 09/758,173
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: 09/383,916
;  PRIOR FILING DATE: 1999-08-26
;  PRIOR APPLICATION NUMBER: 08/487,950
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: primatized peptide sequence
US-10-291-532-12

  Query Match             47.0%;  Score 1271;  DB 14;  Length 476;
  Best Local Similarity   59.8%;  Pred. No. 3.5e-77;
  Matches  274;  Conservative   29;  Mismatches   87;  Indels   68;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |         : |      | |   ||| : | : |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
              :    :  | | : ::   |:  | | | |:   | :|:    ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
              : |     |||   :|  |:  ||             : ::||                |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                   |: | |  | |    |:|       ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 50
US-10-207-655-348
; Sequence 348, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
;   LENGTH: 504
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion polypeptide
US-10-207-655-348

  Query Match             47.0%;  Score 1271;  DB 14;  Length 504;
  Best Local Similarity   55.0%;  Pred. No. 3.8e-77;
  Matches  282;  Conservative   29;  Mismatches   92;  Indels  110;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---KNSN 57
              |:|||  :               ||    :    || | ::| |||      :|   |
Db         19 MSRGVDIQ------------MTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDG 65

Qy         58 QIKILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKE 116
                :|:|    : |   |:|:    || |     | :: | | ||: ||  || |:
Db         66 TVKLL----IYYT---SRLHSGVPSRFSGSGSGTDYSLTIANLQPEDIATYFCQ------ 112

Qy        117 EVQLLVFGLTANSDTHLLQGQSL------------------TLTLESP----PGSSPSV 153
                 |      |    | |:  : |                        |    |    ||:| |
```

```
Db        113 --QGNTLPWTFGGGTKLVTKRELGGGGSGGGGSGGGGSIDEVQLQQSGPELVKPGASMSC 170

Qy        154 QC------------RSPRGKNIQ------------------GGKTLSVSQ-------- 173
              : .           :   |||::                  |  ||:| :
Db        171 KASGYSFTGYIVNWLKQSHGKNLEWIGLINPYKGLTTYNQKFKGKATLTVDKSSSTAYME 230

Qy        174 ---LELQDSGTWTCTVLQNQKKVEFKID-------IVPCPAPEPKSCDKTHTC-----PE 218
                  |  :||  : |          ::  |       :      ||||||||||     ||
Db        231 LLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTVSSDQEPKSCDKTHTCPPCPAPE 290

Qy        219 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 350

Qy        279 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 410

Qy        339 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 470

Qy        399 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||
Db        471 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 503


RESULT 51
US-10-108-260A-4278
; Sequence 4278, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4278
;   LENGTH: 473
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-4278

  Query Match             47.0%;  Score 1270;  DB 15;  Length 473;
  Best Local Similarity   57.6%;  Pred. No. 4.1e-77;
  Matches  279;  Conservative   29;  Mismatches   92;  Indels   84;  Gaps   14;

Qy         13 VLQLALLPAA-TQGNKVVLG----KKGDTVELTCTAS--QKKSIQFHW------KNSNQI 59
                |  :|||     ||  |  |    : | :: |:| ||    |    ||      |    :
Db          8 VFLVALLRGVHCQGQLVQSGGGVVQPGRSLRLSCEASGFSFKFFNMHWVRQAPGKGLEWV 67

Qy         60 KILGNQGS---FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                ::   |:   :      :     |: |: |     |::  |: ||:  | |
Db         68 AVISFDGTKKYYADSVKGRFTVSRDNSRNTLD-----LLMDGLRPEDTAVYSCAKAPFN- 121

Qy        117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                 || |:    |   | ||   :|: |     |||.  :|  |:  ||
Db        122 ----LVRGVHGAFD---LWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 174

Qy        167 ---KTLSVS------------QLELQDSG-----------------TWTCTVLQNQKK 192
                 : ::||                || ||                 |: | |  | |
Db        175 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP 232

Qy        193 VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
                |:|       ||||||||||     |||||||||| ||||||||||||||||||||
Db        233 SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLIPPKPKDTLMISRTPEVTCV 288

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 348

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              ||||||||||||||||||||||||||||||||||:|:||||||||||||||||||||||||
Db        349 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 408

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 468

Qy        428 LSPG 431
              ||||
Db        469 LSPG 472


RESULT 52
US-09-910-600-32
; Sequence 32, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
;  APPLICANT: Longphre, Malinda
;  APPLICANT:  Chang, Han
;  APPLICANT:  Whitney, Gena
;  TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
;  FILE REFERENCE: D0003NP
;  CURRENT APPLICATION NUMBER: US/09/910,600
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: 60/220,139
;  PRIOR FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
;   LENGTH: 619
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: L3a-hIg
US-09-910-600-32

  Query Match             47.0%;  Score 1270;  DB 10;  Length 619;
  Best Local Similarity   57.8%;  Pred. No. 5.8e-77;
  Matches  273;  Conservative   27;  Mismatches   90;  Indels   82;  Gaps   11;

Qy          8 RHLLLVLQLALLPA---ATQGNKVVL-GKKGDTVELTCTASQKKSIQFHWKNSNQIKILG 63
                | |:: :     ||      |||    |  :||  : | | |  :       |
Db        181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSW---------- 230

Qy         64 NQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQ--------- 114
                         | :|  |     |     | :  :|  ||  | |  |::
Db        231 -----------VLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALD 279

Qy        115 ------KEEVQLLVF--------GLTANSDTHLLQGQSLTL---TLESPPGSSPSVQCRS 157
                     | ::::|          |   :   :|:|||| |    |  |||
Db        280 LSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPA--------- 330

Qy        158 PRGKNIQGGKTLSVSQ----------LELQDSGTWTCTVLQ--NQKKVEFKIDIVPCPA 204
                |    | |: || ||           ::::  | :||        : |   : :
Db        331 -RLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV---HD 386

Qy        205 PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 259
              ||||||||||||     ||  | ||||||||||||||||||||||||||||||||||||
Db        387 PEPKSCDKTHTCPPCPAPEFEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 446

Qy        260 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 506

Qy        320 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 566

Qy        380 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 618
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RESULT 53
US-10-467-546-4
; Sequence 4, Application US/10467546
; Publication No. US20040096901A1
; GENERAL INFORMATION:
;  APPLICANT: Gregorio Aversa
;  APPLICANT:  Frank Kolbinger
;  APPLICANT:  Jose M. Carballido Herrera
;  APPLICANT:  Andras Aszodi
;  APPLICANT:  Jose W. Saldanha
;  APPLICANT:  Bruce M. Hall
;  TITLE OF'INVENTION: Therapeutic binding molecules
;  FILE REFERENCE: PCT/EP02/01420
;  CURRENT APPLICATION NUMBER: US/10/467,546
;  CURRENT FILING DATE:  2003-08-08
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: Amino acid sequence of chimeric heavy chain
US-10-467-546-4

  Query Match             47.0%;  Score 1269.5;  DB 16;  Length 448;
  Best Local Similarity   59.3%;  Pred. No. 4.1e-77;
  Matches  275;  Conservative   27;  Mismatches   73;  Indels   89;  Gaps   13;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HW---KNSNQIKILG-----NQGSFLTKGPSKLNDR 79
                | | | :|:::| ||      :  ||   :    :: :|     | |        :| |::
Db         11 LVKPGASVKMSCKASGYTFTNYIIHWVKQEPGQGLEWIGYFNPYNHG-------TKYNEK 63

Qy         80 ADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                 | :|          : : :|  |||  | |              |  |  ||    |
Db         64 FKGRATLTADKSSNTAYMDLSSLTSEDSAIYYCARS-----------GPYAWFDT---WG 109

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
               |  |:|: |     |||   :|  |:  ||             : ::||
Db        110 QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 169

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |    |:|       |||||
Db        170 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK 223

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 283

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 343

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||
Db        344 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 403

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        404 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 447


RESULT 54
US-10-656-769-20
; Sequence 20, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
;  APPLICANT: Varnum, Brian
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Vezina, Chris
;  APPLICANT:  Wong, Lu Min
;  APPLICANT:  Qian, Xueming
;  TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
;  FILE REFERENCE: 01,1554
;  CURRENT APPLICATION NUMBER: US/10/656,769
;  CURRENT FILING DATE:  2003-09-05
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-769-20

  Query Match             47.0%;  Score 1269.5;  DB 16;  Length 469;
  Best Local Similarity   59.0%;  Pred. No. 4.4e-77;
  Matches  276;  Conservative   24;  Mismatches   81;  Indels   87;  Gaps   12;

Qy         25 GNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN----- 77
                | ||  : | :: |:| ||     :   ||       | |          | :| :
Db         27 GGGVV--QPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAGIWNDGINKYHAHSVR 84

Qy         78 -----DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH 132
                     | :|: :|: | | |      : ||:  | |    :      |:|
Db         85 GRFTISRDNSKNTLYLQMNSP------RAEDTAVYYCA---RARSFDWLLFE-------- 127

Qy        133 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------- 172
                ||   :|: |     |||   :|  |:  ||            : ::||
Db        128 -FWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 186

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                     || ||                  |: | |  | |    |:|       |||
Db        187 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 240

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 300

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 360

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 420

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 468


RESULT 55
US-10-108-260A-4073
; Sequence 4073, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4073
;   LENGTH: 472
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-4073

  Query Match             47.0%;  Score 1269;  DB 15;  Length 472;
  Best Local Similarity   59.5%;  Pred. No. 4.8e-77;
  Matches  275;  Conservative   24;  Mismatches   83;  Indels   80;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQ 89
```

```
Db         30 LAQPGGSLRLSCEASGFRLINYAVNWVRQAPGKGLEWISAISGSGGNTHYADSVR----- 84

Qy         90 GNFPL---IIKN--------LKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138

Db         85 GRFTISRDLSKNMVFVQMGSLRAEDTAVYFCAKGNQPR------VDIVASIEN---WGQG 135

Qy        139 LTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------------- 172

Db        136 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 195

Qy        173 QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH 214

Db        196 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTH 249

Qy        215 TC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269

Db        250 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 309

Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329

Db        310 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 369

Qy        330 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 389

Db        370 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 429

Qy        390 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431

Db        430 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471
```

RESULT 56
US-10-108-260A-4285
; Sequence 4285, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4285
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4285

Query Match 46.9%; Score 1268.5; DB 15; Length 471;
Best Local Similarity 57.2%; Pred. No. 5.1e-77;
Matches 277; Conservative 37; Mismatches 85; Indels 85; Gaps 14;

```
Qy         10 LLLVL-----QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQF--HWKN---SNQI 59

Db         10 LLAVISGGQSQVPLVQSGTE-----VKKPGASVNISCKAPGYTFTTFYMHWVRQAPGQGL 64

Qy         60 KILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP---LIIKNLKIEDSDTYICEVEDQKE 116

Db         65 EWMGIRNP--SSGRSSVSQKFEGRLTLTADTSTTTAHMELRNLTSDDTGVYYYCTTTRWKW 122

Qy        117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166

Db        123 VVR--------GEDNYWGQGSLVIVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKD 172

Qy        167 ---KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKK 192

Db        173 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP 230

Qy        193 VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247

Db        231 SNTKVD----EKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 286

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307

Db        287 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 346

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367

Db        347 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 406

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427

Db        407 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 466

Qy        428 LSPG 431

Db        467 LSPG 470
```

RESULT 57
US-10-416-011-2
; Sequence 2, Application US/10416011
; Publication No. US20040126363A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Michael
; APPLICANT: Forman, Stephen
; APPLICANT: Raubitschek, Andrew
; TITLE OF INVENTION: CD19-specific redirected immune cells
; FILE REFERENCE: 1954-338
; CURRENT APPLICATION NUMBER: US/10/416,011
; CURRENT FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD19R: zeta chimeric receptor
US-10-416-011-2

Query Match 46.9%; Score 1268; DB 16; Length 634;
Best Local Similarity 56.2%; Pred. No. 8.1e-77;
Matches 287; Conservative 28; Mismatches 94; Indels 102; Gaps 16;

```
Qy         10 LLLVLQLAL--LP----------AATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---K 54

Db          2 LLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK 61

Qy         55 NSNQIKILGNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVED 113

Db         62 PDGTVKLLIYHTSRLHSGVPSRFSGSGSGT-------DYSLTISNLEQEDIATYFCQQGN 114

Qy        114 QKE-----EVQLLVFGLTANSDTHLLQGQSLT----LTLESPPG-----SSPSVQC---- 155

Db        115 TLPYTFGGGTKLEITGSTSGSGKP-GSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSG 173

Qy        156 ----------RSPRGKNIQ------GGKT----------------------LSVSQLE 175

Db        174 VSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQ 233

Qy        176 LQDSGTWTCTVLQNQKKV----EFKIDI------VPCPAPEPKSCDKTHTC-----PELL 220

Db        234 TDDTAIYYCA-----KHYYYGGSYAMDYWGQGTSVTVSSVEPKSSDKTHTCPPCPAPELL 288

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280

Db        289 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 348

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 340

Db        349 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 408

Qy        341 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 400
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 468

Qy        401 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        469 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 499


RESULT 58
US-10-226-435A-12
; Sequence 12, Application US/10226435A
; Publication No. US20040043418A1
; GENERAL INFORMATION:
;  APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY
;  TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
;  FILE REFERENCE: 8792/293
;  CURRENT APPLICATION NUMBER: US/10/226,435A
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/US01/06191
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 60/184,601
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/254,465
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: 60/254,498
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 442
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized antibodies
US-10-226-435A-12

  Query Match             46.9%;  Score 1267.5;  DB 12;  Length 442;
  Best Local Similarity   59.1%;  Pred. No. 5.5e-77;
  Matches  274;  Conservative   26;  Mismatches   69;  Indels   95;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNS---------NQIKILGNQGSF--LTKGPSKL 76
              | : | :: |:| ||          |           ||  :|| :    :    ||  :
Db         11 LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: :|: | |      :|: ||:  | |                  |: |     |
Db         71 S-RDNAKNTLYLQMN------SLRAEDTAVYYC-----------------ASGD---YWG 103

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |   :|: |     |||   :|  |:  ||             : ::||
Db        104 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 163

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                || ||                   |: | |  | |    |:|       |||||||
Db        164 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 217

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 277

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 337

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 397

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        398 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 59
US-10-120-198B-2
; Sequence 2, Application US/10120198B
; Publication No. US20030215427A1
; GENERAL INFORMATION:
;  APPLICANT: Jensen, Michael
;  TITLE OF INVENTION: CE7-SPECIFIC REDIRECTED IMMUNE CELLS
;  FILE REFERENCE: 1954-337
;  CURRENT APPLICATION NUMBER: US/10/120,198B
;  CURRENT FILING DATE:  2002-04-11
;  PRIOR APPLICATION NUMBER: 60/282,859
;  PRIOR FILING DATE: 2001-04-11
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 631
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: mouse-human chimera
US-10-120-198B-2

  Query Match             46.9%;  Score 1266.5;  DB 15;  Length 631;
  Best Local Similarity   54.2%;  Pred. No. 1e-76;
  Matches  277;  Conservative   39;  Mismatches   84;  Indels  111;  Gaps   14;

Qy          5 VPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQF--HW---KNSNQI 59
              :|    ||: |: |     :     | | | :|:|:| ||      :  ||   :  : :
Db         13 LPHPAFLLIPQVQLQQPGAE-----LVKPGASVKLSCKASGYTFTGYWMHWVKQRPGHGL 67

Qy         60 KILGNQGSFLTKGPSKLNDRADSRRSLW-DQGNFP--LIIKNLKIEDSDTYICEVEDQKE 116
              : :|      : | :  |:|  |: :|  |: :    : :  |  |||  | |  :
Db         68 EWIGEINP--SNGRTNYNERFKSKATLTVDKSSTTAFMQLSGLTSEDSAVYFCARD---- 121

Qy        117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSS------------------------- 150
                :| : | |     ||  |||: |  | |
Db        122 -----YYGTSYNFD---YWGQGTTLTVSSGGGGSGGGGSGGGGSDIQMTQSSSSFSVSLG 173

Qy        151 --PSVQCR-----------------SPR-----------------GKNIQGGKTLSVS 172
                :: |:                 |||                 |       ||:::
Db        174 DRVTITCKANEDINNRLAWYQQTPGNSPRLLISGATNLVTGVPSRFSGSGSGKDYTLTIT 233

Qy        173 QLELQDSGTWTCT-------VLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELL 220
              |: :|  |: |           :  ::| |:        ||||  ||||||      ||||
Db        234 SLQAEDFATYYCQQYWSTPFTFGSGTELEIKV--------EPKSSDKTHTCPPCPAPELL 285

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 345

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 405

Qy        341 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 465

Qy        401 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        466 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 496


RESULT 60
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
;  FILE REFERENCE: P0718P2C1D1C1US
;  CURRENT APPLICATION NUMBER: US/09/925,179
```

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;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 08/466,163
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: PCT/US92/06860
;  PRIOR FILING DATE: 1992-08-14
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
US-09-925-179-68

  Query Match             46.9%;  Score 1266;  DB 10;  Length 451;
  Best Local Similarity   58.6%;  Pred. No. 7.2e-77;
  Matches  273;  Conservative   25;  Mismatches   78;  Indels   90;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND-------- 78
              | : | :: |:|  |        ::|      | |   ||    | :  ||
Db         11 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWMGSITYDGSTNYNDSLKGRITV 70

Qy         79 -RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
               | ||: :      | | : : :||:  | |              ||       |    :
Db         71 SRDDSKNT------FYLQLNSARAEDTAVYYCARGSH-------YFG-------HWHFAV 110

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                  || ||                   |: | |  | |    |:|       |||||
Db        171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 224

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 284

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 344

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        345 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 404

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        405 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 61
US-10-423-299-4
; Sequence 4, Application US/10423299
; Publication No. US20030229212A1
; GENERAL INFORMATION:
;  APPLICANT: FAHRNER, ROBERT
;  APPLICANT:  FOLLMAN, DEBORAH
;  APPLICANT:  LEBRETON, BENEDICTE
;  APPLICANT:  VAN REIS, ROBERT
;  TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
;  FILE REFERENCE: 39766-0121A
;  CURRENT APPLICATION NUMBER: US/10/423,299
;  CURRENT FILING DATE:  2003-04-25
;  PRIOR APPLICATION NUMBER: US 60/375,953
;  PRIOR FILING DATE: 2002-04-26
;  NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized
US-10-423-299-4

  Query Match             46.9%;  Score 1266;  DB 15;  Length 451;
  Best Local Similarity   58.9%;  Pred. No. 7.2e-77;
  Matches  274;  Conservative   28;  Mismatches   75;  Indels   88;  Gaps   13;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKN------SNQIKILG--NQGSFLTKGPSKLNDR-- 79
              | : | :: |:| ||   |   || |          :: :|  :     |:   |  ||
Db         11 LVQPGGSLRLSCAAS-GYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRYNQKFKDRFT 69

Qy         80 ---ADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-LQ 135
                    |: :|: | |       :|: ||:  | |               |:     |:
Db         70 ISVDKSKNTLYLQMN------SLRAEDTAVYYC------------ARGIYFYGTTYFDYW 111

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS---------- 172
              ||   :|: |     |||   :|  |:  ||             : ::||
Db        112 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 171

Qy        173 ---QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211
                   || ||                   |: | |  | |    |:|       ||||||
Db        172 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD 225

Qy        212 KTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 266
              |||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 285

Qy        267 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 345

Qy        327 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 386
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        346 QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 405

Qy        387 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        406 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 450


RESULT 62
US-10-020-786-9
; Sequence 9, Application US/10020786
; Publication No. US20030073164A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Laura C.
;  APPLICANT:  Klimowski, Laura
;  APPLICANT:  Reilly, Dorothea
;  APPLICANT:  Yansura, Daniel G.
;  TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: P1793R1
;  CURRENT APPLICATION NUMBER: US/10/020,786
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/256,164
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: anti-TF heavy chain
US-10-020-786-9

  Query Match             46.9%;  Score 1266;  DB 14;  Length 470;
  Best Local Similarity   58.8%;  Pred. No. 7.6e-77;
```

```
  Matches  275;  Conservative   26;  Mismatches   69;  Indels   98;  Gaps   14;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILG-NQGSFLTKGPSKLNDRA 80
              | : | :: |:| ||    |    ||       |    : ::   ||:  |    |  |||
Db         34 LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA 91

Qy         81 -----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-- 133
                   :|: : : | |       :|: ||:  | |                    ||
Db         92 TISADNSKNTAYLQMN------SLRAEDTAVYYCA-----------------RDTAAYF 127

Qy        134 -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------- 172
               ||   :|: |    |||   :|  |:  ||             : ::||
Db        128 DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 187

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                   || ||                   |: | |  | |    |:|       |||
Db        188 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 241

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        242 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 301

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 361

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||
Db        362 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 421

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469


RESULT 63
US-10-227-694-5
; Sequence 5, Application US/10227694
; Publication No. US20030077739A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Laura
;  APPLICANT:  Andersen, Dana
;  TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
;  FILE REFERENCE: P1867R1
;  CURRENT APPLICATION NUMBER: US/10/227,694
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/315,209
;  PRIOR FILING DATE: 2001-08-27
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-227-694-5

  Query Match           46.9%;  Score 1266;  DB 14;  Length 470;
  Best Local Similarity   58.8%;  Pred. No. 7.6e-77;
  Matches  275;  Conservative   26;  Mismatches   69;  Indels   98;  Gaps   14;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILG-NQGSFLTKGPSKLNDRA 80
              | : | :: |:| ||    |    ||       |    : ::   ||:  |    |  |||
Db         34 LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA 91

Qy         81 -----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-- 133
                   :|: : : | |       :|: ||:  | |                    ||
Db         92 TISADNSKNTAYLQMN------SLRAEDTAVYYCA-----------------RDTAAYF 127

Qy        134 -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------- 172
               ||   :|: |    |||   :|  |:  ||             : ::||
Db        128 DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 187

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                   || ||                   |: | |  | |    |:|       |||
Db        188 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 241

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        242 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 301

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 361

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||
Db        362 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 421

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469


RESULT 64
US-09-848-832-3
; Sequence 3, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
;  APPLICANT: Hooper, Douglas
;  APPLICANT:  Dietzschold, Bernhard
;  TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
;  FILE REFERENCE: HO01.NP0002
;  CURRENT APPLICATION NUMBER: US/09/848,832
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: 60/204,518
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-848-832-3

  Query Match           46.9%;  Score 1266;  DB 10;  Length 474;
  Best Local Similarity   59.1%;  Pred. No. 7.6e-77;
  Matches  276;  Conservative   32;  Mismatches   71;  Indels   88;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP 73
              | : | :: |:| ||            |       | ::  |   |:  ::|    ||
Db         30 LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR 86

Qy         74 SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                :: | :|: :|: | |       :|: ||:  | |    :  || ::|  |    |
Db         87 FTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD--- 132

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        133 YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 192

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                  || ||                   |: | |  | |    |:|       ||||
Db        193 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS 246

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 306

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 366

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||
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Db        367 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 426

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473


RESULT 65
US-10-225-108A-3
; Sequence 3, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
;  APPLICANT: HOOPER, Craig
;  APPLICANT:  DIETZSCHOLD, Bernhard
;  TITLE OF INVENTION: Recombinant Antibodies, and Compositions
;  TITLE OF INVENTION:  and Methods for Making Them
;  FILE REFERENCE: 8321-110
;  CURRENT APPLICATION NUMBER: US/10/225,108A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: US 09/848,832
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/204,518
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: US 60/314,023
;  PRIOR FILING DATE: 2001-08-21
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-108A-3

  Query Match             46.9%;  Score 1266;  DB 14;  Length 474;
  Best Local Similarity   59.1%;  Pred. No. 7.6e-77;
  Matches  276;  Conservative   32;  Mismatches   71;  Indels   88;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS------------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP 73
              | : | :: |:| ||             |       | ::  |   |:  ::|    ||
Db         30 LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR 86

Qy         74 SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                :: | :|: :|: | |      :|: ||:  | |    :  || ::|  |    |
Db         87 FTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD--- 132

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS-------- 172
                ||   :|: |     |||   :|  |:  ||             : ::||
Db        133 YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 192

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                    || ||                 |: | |  | |    |:|       ||||
Db        193 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS 246

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 306

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 366

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              |||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        367 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 426

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473


RESULT 66
US-10-461-148-1
; Sequence 1, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
;  APPLICANT: Dietzschold, Bernhard
;  APPLICANT:  Hooper, Douglas C.
;  TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS FOR MAKING AND USING THE SAME
;  FILE REFERENCE: 8321-110CI1-185685
;  CURRENT APPLICATION NUMBER: US/10/461,148
;  CURRENT FILING DATE:  2003-06-13
;  PRIOR APPLICATION NUMBER: US 10/225,108
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/314,023
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 09/848,832
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/204,518
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Human
US-10-461-148-1

  Query Match             46.9%;  Score 1266;  DB 15;  Length 474;
  Best Local Similarity   59.1%;  Pred. No. 7.6e-77;
  Matches  276;  Conservative   32;  Mismatches   71;  Indels   88;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS------------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP 73
              | : | :: |:| ||             |       | ::  |   |:  ::|    ||
Db         30 LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR 86

Qy         74 SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                :: | :|: :|: | |      :|: ||:  | |    :  || ::|  |    |
Db         87 FTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD--- 132

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS-------- 172
                ||   :|: |     |||   :|  |:  ||             : ::||
Db        133 YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 192

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                    || ||                 |: | |  | |    |:|       ||||
Db        193 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS 246

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 306

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 366

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              |||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        367 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 426

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473


RESULT 67
US-10-207-655-240
; Sequence 240, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
```

```
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
;   LENGTH: 500
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion polypeptide
US-10-207-655-240

  Query Match            46.9%;  Score 1266;  DB 14;  Length 500;
  Best Local Similarity  56.3%;  Pred. No. 8.2e-77;
  Matches  274;  Conservative   27;  Mismatches   94;  Indels   92;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||         |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || ||    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:               :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :       :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 ID-------IVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV 244
               |       :      ||||||||||     ||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV 312

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 372

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 432

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 492

Qy        425 SLSLSPG 431
              |||||||
Db        493 SLSLSPG 499


RESULT 68
US-10-207-655-398
; Sequence 398, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 398
;   LENGTH: 500
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion polypeptide
US-10-207-655-398

  Query Match            46.9%;  Score 1266;  DB 14;  Length 500;
  Best Local Similarity  56.3%;  Pred. No. 8.2e-77;
  Matches  274;  Conservative   27;  Mismatches   94;  Indels   92;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||         |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || ||    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:               :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :       :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 ID-------IVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV 244
               |       :      ||||||||||     ||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSSDQEPKSCDKTHTCPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEV 312

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 372

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 432

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 492

Qy        425 SLSLSPG 431
              |||||||
Db        493 SLSLSPG 499


RESULT 69
US-10-071-485-67
; Sequence 67, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
;  TITLE OF INVENTION:  SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/10/071,485
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: 09/485,737
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
;   LENGTH: 468
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

  Query Match            46.8%;  Score 1265.5;  DB 14;  Length 468;
  Best Local Similarity  57.2%;  Pred. No. 8.1e-77;
```

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  Matches  277;  Conservative   31;  Mismatches   79;  Indels   97;  Gaps   13;

Qy         11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70
              ::: |: |: : ::    | | | :|:::| ||      |     | :|    ||
Db         17 VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L 65

Qy         71 KGPSKLNDRADSRRSLWD-QGNFP-----------LIIKNLKIEDSDTYICEVEDQKEEV 118
              |    :|        : | :| |            | | :|| ||: || |
Db         66 KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC--------- 116

Qy        119 QLLVFGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                     |    : :   ||  |:|: |      |||   :|  |:  ||
Db        117 --------ARRGFYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 168

Qy        167 ---KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKK 192
                 : ::||              || ||                    |: | |  | |
Db        169 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP 226

Qy        193 VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
                |:|       ||||||||||      ||||||||||||||||||||||||||||||
Db        227 SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 282

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 342

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              |||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||||||
Db        343 VSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 402

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 462

Qy        428 LSPG 431
              ||||
Db        463 LSPG 466


RESULT 70
US-10-071-485-90
; Sequence 90, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
;  TITLE OF INVENTION:  SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/10/071,485
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: 09/485,737
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

  Query Match           46.8%;  Score 1265.5;  DB 14;  Length 711;
  Best Local Similarity   57.2%;  Pred. No. 1.4e-76;
  Matches  277;  Conservative   31;  Mismatches   79;  Indels   97;  Gaps   13;

Qy         11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70
              ::: |: |: : ::    | | | :|:::| ||      |     | :|    ||
Db         17 VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L 65

Qy         71 KGPSKLNDRADSRRSLWD-QGNFP-----------LIIKNLKIEDSDTYICEVEDQKEEV 118
              |    :|        : | :| |            | | :|| ||: || |
Db         66 KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC--------- 116

Qy        119 QLLVFGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                     |    : :   ||  |:|: |      |||   :|  |:  ||
Db        117 --------ARRGFYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 168

Qy        167 ---KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKK 192
                 : ::||              || ||                    |: | |  | |
Db        169 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP 226

Qy        193 VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
                |:|       ||||||||||      ||||||||||||||||||||||||||||||
Db        227 SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 282

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 342

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              |||||||| ||||||||||||||||||||||||:|:||||||||||||||||||||||||||
Db        343 VSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 402

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 462

Qy        428 LSPG 431
              ||||
Db        463 LSPG 466


RESULT 71
US-10-408-901-42
; Sequence 42, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathwa
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-42

  Query Match           46.8%;  Score 1265;  DB 16;  Length 445;
  Best Local Similarity   59.0%;  Pred. No. 8.2e-77;
  Matches  271;  Conservative   27;  Mismatches   71;  Indels   90;  Gaps   12;

Qy         34 GDTVELTCTASQ--KKSIQFHW------KNSNQIKILGNQG----SFLTKGPSKLNDRAD 81
              | :: |:|  |:    :    ||      |     :  :|: |    :    ||   :: |
Db         15 GGSLRLSCVGSRFTFSAYPMHWVRQAPGKGLEWVSGIGSGGGTNYADSVKGRFTIS-RDT 73

Qy         82 SRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL 141
              :: ||: | |      :|: ||   | |                    ::    ||  :
Db         74 AKNSLYLQMN------SLRAEDMAVYYC---------------ARGRNSFDYWGQGTLV 111
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```
Qy        142 TLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLE 175
              |: |     |||   :|  |:  ||             : ::||
Db        112 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 171

Qy        176 LQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC- 216
              || ||                 |: | |  | |    |:|       ||||||||||
Db        172 LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP 225

Qy        217 ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 285

Qy        273 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 345

Qy        333 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 405

Qy        393 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        406 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 444
```

```
RESULT 72
US-10-411-037-56
; Sequence 56, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
;  TITLE OF INVENTION:  GALACTOSIDASE A
;  FILE REFERENCE: 040853-01-5082
;  CURRENT APPLICATION NUMBER: US/10/411,037
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-037-56

  Query Match             46.8%;  Score 1265;  DB 12;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::    ||       :   | : |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67
```

```
Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              :|          : : :|: ||:  | |  |               |       ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QL 174
              :|: |     |||   :|  |:  ||             : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
              || ||                 |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
```

```
RESULT 73
US-10-411-026-56
; Sequence 56, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5053
;  CURRENT APPLICATION NUMBER: US/10/411,026
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-026-56

  Query Match             46.8%;  Score 1265;  DB 12;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::    ||       :   | : |::   |
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```
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              :|          : : :|: ||:  | |   |              |        ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||             : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
              || ||                 |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
```

RESULT 74
US-10-410-962-56
; Sequence 56, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-56

Query Match 46.8%; Score 1265; DB 16; Length 448;
Best Local Similarity 58.7%; Pred. No. 8.3e-77;
Matches 270; Conservative 26; Mismatches 80; Indels 84; Gaps 11;

```
Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||       :   |      ::     ||       :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              :|          : : :|: ||:  | |   |              |        ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||             : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
              || ||                 |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
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RESULT 75
US-10-411-049-56
; Sequence 56, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: ALPHA
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-56

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  Query Match             46.8%;  Score 1265;  DB 16;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::    ||        :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              :|          : : :|: ||:  | |   |              |       ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||             : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448


RESULT 76
US-10-410-930-56
; Sequence 56, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
;  TITLE OF INVENTION:  BETA
;  FILE REFERENCE: 040853-01-5056
;  CURRENT APPLICATION NUMBER: US/10/410,930
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-930-56

  Query Match             46.8%;  Score 1265;  DB 16;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::    ||        :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              :|          : : :|: ||:  | |   |              |       ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||             : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448


RESULT 77
US-10-410-997-56
; Sequence 56, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
;  TITLE OF INVENTION:  FSH
;  FILE REFERENCE: 040853-01-5059
;  CURRENT APPLICATION NUMBER: US/10/410,997
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-997-56

  Query Match            46.8%;  Score 1265;  DB 16;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::     ||      :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
               :|          : : :|: ||:  | |   |              |       ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||            : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                |: | |  | |    |:|      ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448


RESULT 78
US-10-411-012-56
; Sequence 56, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryne
;  TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5051
;  CURRENT APPLICATION NUMBER: US/10/411,012
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-411-012-56

  Query Match            46.8%;  Score 1265;  DB 16;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::     ||      :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
               :|          : : :|: ||:  | |   |              |       ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||            : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                |: | |  | |    |:|      ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448


RESULT 79
US-10-287-994-56
; Sequence 56, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Bowe, Caryn
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
;  FILE REFERENCE: 040853-01-5052-00
;  CURRENT APPLICATION NUMBER: US/10/287,994
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
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;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-994-56

  Query Match             46.8%;  Score 1265;  DB 16;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::    ||       :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
               :|          : : :|: ||:  | |   |              |      ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||              : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448


RESULT 80
US-10-410-913-56
; Sequence 56, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5081
;  CURRENT APPLICATION NUMBER: US/10/410,913
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-410-913-56

  Query Match             46.8%;  Score 1265;  DB 16;  Length 448;
  Best Local Similarity   58.7%;  Pred. No. 8.3e-77;
  Matches  270;  Conservative   26;  Mismatches   80;  Indels   84;  Gaps   11;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG------SFLTKGPSKLNDRADSR 83
              | | :|:::| ||      :   |     ::    ||       :   | :  |::   |
Db         13 KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR 67

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
               :|          : : :|: ||:  | |   |              |      ||
Db         68 VTLTVDESTNTAYMELSSLRSEDTAVYFCARRD------------GNYGWFAYWGQGTL 114

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QL 174
              :|: |     |||   :|  |:  ||              : ::||
Db        115 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Qy        175 ELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
               || ||                |: | |  | |    |:|       ||||||||||
Db        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC 228

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 348

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 408

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448


RESULT 81
US-09-773-877A-18
; Sequence 18, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877A
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(2-3)-Fc (Mut3)
US-09-773-877A-18

  Query Match             46.8%;  Score 1265;  DB 12;  Length 462;
  Best Local Similarity   65.7%;  Pred. No. 8.6e-77;
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  Matches  255;  Conservative   24;  Mismatches   71;  Indels   38;  Gaps    7;

Qy          81 DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVE----------DQKEEVQLLVFGLTANS 129
               | :| :||      || |   ::      ||             ::   ::   ::
Db          75 DGKRIIWDSRK-GFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPR 133

Qy         130 DTHLLQGQSLTL--TLESPPGSSPSVQCRSPRGKNIQGG---------------KTLSV 171
                 ||:| :| |  |  :|  :   :    |  || :                  |::
Db         134 PVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTI 193

Qy         172 SQLELQDSGTWTCTVLQNQ--KKVEFKIDIVPCPAP-EPKSCDKTHTC-----PELLGGP 223
                ::: :| | :|| |      | |   : |      | ||||||||||     |||||||
Db         194 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 253

Qy         224 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 283
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         254 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 313

Qy         284 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         314 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 373

Qy         344 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 433

Qy         404 QGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               ||||||||||||||||||||||||||||
Db         434 QGNVFSCSVMHEALHNHYTQKSLSLSPG 461


RESULT 82
US-09-773-877A-12
; Sequence 12, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877A
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 567
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt(1-3)-Fc
US-09-773-877A-12

  Query Match           46.8%;  Score 1265;  DB 12;  Length 567;
  Best Local Similarity   65.7%;  Pred. No. 1.1e-76;
  Matches  255;  Conservative   24;  Mismatches   71;  Indels   38;  Gaps    7;

Qy          81 DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVE----------DQKEEVQLLVFGLTANS 129
               | :| :||      || |   ::      ||             ::   ::   ::
Db         180 DGKRIIWDSRK-GFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPR 238

Qy         130 DTHLLQGQSLTL--TLESPPGSSPSVQCRSPRGKNIQGG---------------KTLSV 171
                 ||:| :| |  |  :|  :   :    |  || :                  |::
Db         239 PVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTI 298

Qy         172 SQLELQDSGTWTCTVLQNQ--KKVEFKIDIVPCPAP-EPKSCDKTHTC-----PELLGGP 223
                ::: :| | :|| |      | |   : |      | ||||||||||     |||||||
Db         299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy         224 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 283
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy         284 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy         344 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy         404 QGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               ||||||||||||||||||||||||||||
Db         539 QGNVFSCSVMHEALHNHYTQKSLSLSPG 566


RESULT 83
US-09-875-338-9
; Sequence 9, Application US/09875338
; Patent No. US20020095024A1
; GENERAL INFORMATION:
;  APPLICANT: MIKESELL, GLEN E.
;  APPLICANT:  CHANG, HAN
;  APPLICANT:  FINGER, JOSHUA N.
;  APPLICANT:  YANG, GUCHEN
;  APPLICANT:  LU, PIN
;  APPLICANT:  ZHOU, XIA-DI
;  APPLICANT:  PEACH, ROBERT
;  TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
;  TITLE OF INVENTION:  IMMUNOMODULATION
;  FILE REFERENCE: 3053-4071US2
;  CURRENT APPLICATION NUMBER: US/09/875,338
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: 60/272,107
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/209,811
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 698
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: fusion construct
US-09-875-338-9

  Query Match           46.8%;  Score 1265;  DB 9;  Length 698;
  Best Local Similarity   67.8%;  Pred. No. 1.5e-76;
  Matches  261;  Conservative   18;  Mismatches   57;  Indels   49;  Gaps    7;

Qy          89 QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES--- 145
               |||  | :: ::: |  :: |        | :  ||  | |          ::|||
Db         320 QGNASLRLQRVRVADEGSFTC-------FVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKD 372

Qy         146 -PPGSSPSVQCRSPRG-----------------------KNIQG-GKTLSVSQLELQD 178
                 || : :: | | ||                      | ||     || :: |
Db         373 LRPGDTVTITCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGA 432

Qy         179 SGTWTC----TVLQNQKKVEFKIDIVPCPAP---EPKSCDKTHTC-----PELLGGPSVF 226
               :||::|    |||         |   |   |   ||||||||||     |||||||||
Db         433 NGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEFEPKSCDKTHTCPPCPAPELLGGPSVF 492

Qy         227 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 286
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         493 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 552

Qy         287 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         553 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 612

Qy         347 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 406
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         613 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 672

Qy         407 VFSCSVMHEALHNHYTQKSLSLSPG 431
               |||||||||||||||||||||||||
Db         673 VFSCSVMHEALHNHYTQKSLSLSPG 697
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Db        673 VFSCSVMHEALHNHYTQKSLSLSPG 697


RESULT 84
US-10-077-023-9
; Sequence 9, Application US/10077023
; Publication No. US20030031675A1
; GENERAL INFORMATION:
;  APPLICANT: MIKESELL, GLEN E.
;  APPLICANT:  CHANG, HAN
;  APPLICANT:  FINGER, JOSHUA N.
;  APPLICANT:  YANG, GUCHEN
;  APPLICANT:  LU, PIN
;  APPLICANT:  ZHOU, XIA-DI
;  APPLICANT:  PEACH, ROBERT
;  TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
;  TITLE OF INVENTION:  IMMUNOMODULATION
;  FILE REFERENCE: 3053-4071US3
;  CURRENT APPLICATION NUMBER: US/10/077,023
;  CURRENT FILING DATE:  2002-02-15
;  PRIOR APPLICATION NUMBER: 60/272,107
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/209,811
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 138
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 698
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: fusion construct
US-10-077-023-9

  Query Match             46.8%;  Score 1265;  DB 14;  Length 698;
  Best Local Similarity   67.8%;  Pred. No. 1.5e-76;
  Matches  261;  Conservative   18;  Mismatches   57;  Indels   49;  Gaps    7;

Qy          89 QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES--- 145
               |||  | :: ::: |  :: |        | :  ||  | |          ::|||
Db         320 QGNASLRLQRVRVADEGSFTC-------FVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKD 372

Qy         146 -PPGSSPSVQCRSPRG------------------------KNIQG-GKTLSVSQLELQD 178
                || : :: | | ||                        | ||    || :: |
Db         373 LRPGDTVTITCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGA 432

Qy         179 SGTWTC----TVLQNQKKVEFKIDIVPCPAP---EPKSCDKTHTC-----PELLGGPSVF 226
               :||::|     |||         |   |   |  ||||||||||     ||||||||||
Db         433 NGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEFEPKSCDKTHTCPPCPAPELLGGPSVF 492

Qy         227 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 286
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         493 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 552

Qy         287 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         553 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 612

Qy         347 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 406
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         613 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 672

Qy         407 VFSCSVMHEALHNHYTQKSLSLSPG 431
               |||||||||||||||||||||||||
Db         673 VFSCSVMHEALHNHYTQKSLSLSPG 697


RESULT 85
US-09-773-877A-20
; Sequence 20, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
;  APPLICANT: Xia, Yu-Ping et al.
;  TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
;  FILE REFERENCE: REG 710b
;  CURRENT APPLICATION NUMBER: US/09/773,877A
;  CURRENT FILING DATE:  2001-01-31
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 567
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Flt1(1-3 R->N)-Fc (Mut4)
US-09-773-877A-20

  Query Match             46.8%;  Score 1264;  DB 12;  Length 567;
  Best Local Similarity   65.7%;  Pred. No. 1.3e-76;
  Matches  255;  Conservative   23;  Mismatches   72;  Indels   38;  Gaps    7;

Qy          81 DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVE-----------DQKEEVQLLVFGLTANS 129
               | :| :||         || |    ::      ||           ::   ::   ::
Db         180 DGKRIIWDSRK-GFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVQISTPR 238

Qy         130 DTHLLQGQSLTL--TLESPPGSSPSVQCRSPRGKNIQGG---------------KTLSV 171
                  ||:| :| |  |  :|  :   :    | ||                    |::
Db         239 PVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKNASVRRRIDQSNSHANIFYSVLTI 298

Qy         172 SQLELQDSGTWTCTVLQNQ--KKVEFKIDIVPCPAP-EPKSCDKTHTC-----PELLGGP 223
                ::: :| | :|| |       | |   : |     | ||||||||||     |||||||
Db         299 DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP 358

Qy         224 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 283
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418

Qy         284 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 478

Qy         344 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538

Qy         404 QGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               ||||||||||||||||||||||||||||
Db         539 QGNVFSCSVMHEALHNHYTQKSLSLSPG 566


RESULT 86
US-09-796-848A-37
; Sequence 37, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James F.
;  APPLICANT:  Johnson, Leslie S.
;  APPLICANT:  Huse, William D.
;  APPLICANT:  Wu, Herren
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
;  TITLE OF INVENTION:  Producing Them
;  FILE REFERENCE: 469201-526
;  CURRENT APPLICATION NUMBER: US/09/796,848A
;  CURRENT FILING DATE:  2001-10-30
;  PRIOR APPLICATION NUMBER: U.S. 60/186,252
;  PRIOR FILING DATE: 2000-03-01
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
```

```
;   OTHER INFORMATION: high potency antibody.
US-09-796-848A-37

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |              :   |    :: : | |          : :
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   || |         :    | : |:   |: || |  :       ::|    :
Db         60 DYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |     ||| . :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 87
US-09-796-848A-45
; Sequence 45, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James F.
;  APPLICANT:  Johnson, Leslie S.
;  APPLICANT:  Huse, William D.
;  APPLICANT:  Wu, Herren
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
;  TITLE OF INVENTION:  Producing Them
;  FILE REFERENCE: 469201-526
;  CURRENT APPLICATION NUMBER: US/09/796,848A
;  CURRENT FILING DATE:  2001-10-30
;  PRIOR APPLICATION NUMBER: U.S. 60/186,252
;  PRIOR FILING DATE: 2000-03-01
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
;   OTHER INFORMATION: high potency antibody.
US-09-796-848A-45

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |              :   |    :: : | |          : :
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   || |         :    | : |:   |: || |  :       ::|    :
Db         60 HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |     ||| . :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 88
US-09-996-288-220
; Sequence 220, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-220

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |              :   |    :: : | |          : :
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   || |         :    | : |:   |: || |  :       ::|    :
Db         60 DYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |     ||| . :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220
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Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 89
US-09-996-288-226
; Sequence 226, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 226
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-226

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |              :   |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                 || |         :   | : |:   |: || |  :        ::|    :
Db         60 HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
              : ||  |:|: |     |||   :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 90
US-09-996-288-232
; Sequence 232, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-232

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |              :   |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||         :   | : |:   |: || |  :        ::|    :
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNWYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
              : ||  |:|: |     |||   :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 91
US-09-996-288-234
; Sequence 234, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
```

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;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-234

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||           :    | : |:   |: || |  :        ::|    :
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNWYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
              : ||  |:|: |     |||   :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 92
US-09-996-288-236
; Sequence 236, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 236
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-236

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||           :    | : |:   |: || |  :        ::|    :
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNWYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
              : ||  |:|: |     |||   :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 93
US-09-996-288-238
; Sequence 238, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-238

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   26;  Mismatches   75;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||           :    | : |:   |: || |     :: :    |
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYC----ARDMITNFYFD------- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
              : ||  |:|: |     |||   :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 94
US-09-996-288-242
; Sequence 242, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-242

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   26;  Mismatches   75;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |         :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||             :    | : |:   |: || |     :: :    |
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYC----ARDMITNFYFD------- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------ 172
                : ||  |:|: |     |||   :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 95
US-09-996-288-244
; Sequence 244, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-244

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   26;  Mismatches   75;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |         :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||             :    | : |:   |: || |     :: :    |
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYC----ARDMITNFYFD------- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------ 172
                : ||  |:|: |     |||   :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                   |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 96
US-09-996-288-246
; Sequence 246, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 246
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-246

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   26;  Mismatches   75;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |                :   |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSL---------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   ||           :    | : |:   |: || |     :: :    |
Db         60 DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYC----ARDMITNFYFD------- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |      |||   :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 97
US-09-996-288-252
; Sequence 252, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-252

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |                :   |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                 || |           :    | : |:   |: || |  :          ::|    :
Db         60 HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |      |||   :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 98
US-09-996-288-254
; Sequence 254, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylax
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 254
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-254

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |   |: |||| |                :   |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                 || |           :    | : |:   |: || |  :          ::|    :
Db         60 HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |      |||   :|  |:  ||             : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280
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Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 99
US-09-996-288-256
; Sequence 256, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-047-999
;  CURRENT APPLICATION NUMBER: US/09/996,288
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 256
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-288-256

  Query Match             46.8%;  Score 1263.5;  DB 9;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |          :|:
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                 || |          :    | : |:   |: || |  :         ::|    :
Db         60 HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |     |||  :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     |||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 100
US-09-996-265-220
; Sequence 220, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
;  APPLICANT: Young, James
;  APPLICANT:  Scott, Koenig
;  APPLICANT:  Leslie, Johnson
;  TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
;  TITLE OF INVENTION:  and Treatment
;  FILE REFERENCE: 10271-048-999
;  CURRENT APPLICATION NUMBER: US/09/996,265
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-265-220

  Query Match             46.8%;  Score 1263.5;  DB 10;  Length 450;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-76;
  Matches  271;  Conservative   27;  Mismatches   74;  Indels   97;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL---------NDRA 80
              | |    |: |||| |              :    |    :: : | |          : :
Db         11 LVKPTQTLTLTCTFS-----------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKK 59

Qy         81 DSRRSLWD---------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                 || |          :    | : |:   |: || |  :         ::|    :
Db         60 DYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD--------MIFNFYFD--- 108

Qy        132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------ 172
               : ||  |:|: |     |||  :|  |:  ||              : ::||
Db        109 --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 166

Qy        173 -------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                    || ||                    |: | |  | |    |:|       ||
Db        167 TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP 220

Qy        208 KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |||||||||     |||||||||||||||||||||||||||||||||||||||||||||||
Db        221 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 280

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 340

Qy        323 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              ||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        341 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 400

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


Search completed: August  3, 2004, 13:48:10
Job time : 51.3363 secs
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OM protein - protein search, using sw model

Run on: August 3, 2004, 12:50:09 ; Search time 52.0897 Seconds
(without alignments)
2777.216 Million cell updates/sec

Title: SEQ8
Perfect score: 2702
Sequence: 1 MNRGVPFRHLLLVLQLALLP.....VISFLLGLGLGVACVLARTR 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 125 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2216	82.0	435	2	AAR26530	Aar26530 Sequence
2	2188.5	81.0	450	6	AAE37574	Aae37574 Human D1D
3	2176	80.5	534	2	AAR26531	Aar26531 Sequence
4	2169	80.3	449	6	AAE37576	Aae37576 Human FD1
5	2126.5	78.7	631	1	AAP93009	Aap93009 Genetic c
6	2126.5	78.7	631	3	AAB19508	Aab19508 CD4-IgG1
7	2126.5	78.7	631	3	AAY51079	Aay51079 Human fus
8	2126.5	78.7	631	3	AAY59169	Aay59169 CD4-Ig fu
9	2122	78.5	432	2	AAR26782	Aar26782 CD4-gamma
10	2122	78.5	432	2	AAR46678	Aar46678 CD4-gamma
11	2122	78.5	432	3	AAY85079	Aay85079 Human CD4
12	2122	78.5	432	4	AAB67322	Aab67322 CD4-gamma
13	2122	78.5	432	4	AAB80883	Aab80883 Human CD4
14	2122	78.5	432	6	ABG71122	Abg71122 CD4-gamma
15	2085	77.2	530	2	AAR26783	Aar26783 CD4-IgG2
16	2085	77.2	530	3	AAY85080	Aay85080 CD4-IgG2
17	2085	77.2	530	4	AAB67323	Aab67323 CD4-IgG2
18	2085	77.2	530	4	AAB80884	Aab80884 Human CD4
19	2085	77.2	530	6	ABG71123	Abg71123 CD4-immun
20	2081	77.0	616	3	AAY51082	Aay51082 Human fus
21	2081	77.0	616	3	AAY59172	Aay59172 CD4-Ig fu
22	2079.5	77.0	729	1	AAP93008	Aap93008 Genetic c
23	2079.5	77.0	729	3	AAB19507	Aab19507 CD4-IgG1
24	2079.5	77.0	729	3	AAY59168	Aay59168 CD4-Ig fu
25	2075	76.8	530	2	AAR46679	Aar46679 CD4-IgG2
26	2069.5	76.6	729	3	AAY51078	Aay51078 Human fus
27	2056	76.1	614	1	AAP93012	Aap93012 Genetic c
28	1999	74.0	616	3	AAB19511	Aab19511 CD4-IgG1
29	1647.5	61.0	410	2	AAW35860	Aaw35860 Human CD4
30	1546	57.2	343	2	AAR20634	Aar20634 Chimeric
31	1338.5	49.5	254	2	AAR89441	Aar89441 IgG1 hing
32	1332.5	49.3	254	2	AAR78667	Aar78667 IgG1 hing
33	1327.5	49.1	400	7	ADD13790	Add13790 Plasmid p
34	1315	48.7	401	7	ADD13781	Add13781 Plasmid p
35	1287.5	47.6	437	6	ABJ37104	Abj37104 Concatame
36	1287	47.6	461	2	AAR42162	Aar42162 Anti-HIV-
37	1285.5	47.6	449	5	AAO18400	Aao18400 Mature hu
38	1284.5	47.5	459	2	AAR42066	Aar42066 Human ant
39	1282.5	47.5	446	2	AAW05829	Aaw05829 Humanised
40	1282.5	47.5	617	6	ABJ37106	Abj37106 Concatame
41	1282.5	47.5	617	6	ABJ37108	Abj37108 Concatame
42	1282	47.4	582	4	AAB81991	Aab81991 Gangliosi
43	1280.5	47.4	461	4	AAU07745	Aau07745 Humanised
44	1280.5	47.4	475	2	AAW11639	Aaw11639 Human ant
45	1280	47.4	473	5	ABG70743	Abg70743 Mouse/hum
46	1280	47.4	476	2	AAW88464	Aaw88464 Monoclona
47	1279.5	47.4	448	5	AAM49203	Aam49203 Humanised
48	1279.5	47.4	452	2	AAY30201	Aay30201 Heavy cha
49	1279	47.3	470	3	AAY44721	Aay44721 Human imm
50	1279	47.3	492	7	ADD25783	Add25783 Binding d
51	1278.5	47.3	581	4	AAB81972	Aab81972 Gangliosi
52	1277	47.3	543	7	ADD25784	Add25784 Binding d
53	1275.5	47.2	461	6	ABR39847	Abr39847 Hu266 N56
54	1275.5	47.2	461	6	ABR39843	Abr39843 Hu266 N56
55	1275.5	47.2	579	6	AAE33444	Aae33444 KS antibo
56	1275	47.2	595	2	AAW86003	Aaw86003 Anti-5T4
57	1274.5	47.2	445	6	AAO31101	Aao31101 Human A2-
58	1274.5	47.2	461	6	ABR39844	Abr39844 Hu266 N56
59	1274.5	47.2	461	6	ABR39848	Abr39848 Hu266 N56
60	1274.5	47.2	473	4	AAB36206	Aab36206 Human imm
61	1274	47.2	468	5	AAE27928	Aae27928 Human C5E
62	1274	47.2	468	6	ABB82837	Abb82837 Antibody
63	1273.5	47.1	444	6	AAE35327	Aae35327 Humanised
64	1273.5	47.1	444	6	AAE34876	Aae34876 BIWA4/8 a
65	1273.5	47.1	475	2	AAR93553	Aar93553 Monoclona
66	1273.5	47.1	475	2	AAW11641	Aaw11641 Human ant
67	1273.5	47.1	497	3	AAY97172	Aay97172 Human FGF
68	1273.5	47.1	525	3	AAY97171	Aay97171 Human FGF
69	1273.5	47.1	622	3	AAY97170	Aay97170 Human FGF
70	1273	47.1	592	4	AAB83838	Aab83838 Amino aci
71	1272.5	47.1	465	7	ADE64199	Ade64199 LL2HCF pr
72	1272	47.1	476	4	AAB49243	Aab49243 Chimeric
73	1271.5	47.1	453	2	AAY50151	Aay50151 Antibody
74	1271.5	47.1	499	5	ABG31025	Abg31025 Synthetic
75	1271.5	47.1	499	7	ADD25587	Add25587 Binding d
76	1271.5	47.1	499	7	ADD25454	Add25454 Binding d
77	1271	47.0	468	6	ABP58275	Abp58275 Humanised
78	1271	47.0	472	2	AAR93166	Aar93166 Anti-rhes
79	1271	47.0	476	2	AAW01822	Aaw01822 Primatise
80	1271	47.0	476	2	AAW63765	Aaw63765 Macaque p
81	1271	47.0	476	5	AAU11646	Aau11646 Protein s
82	1271	47.0	504	7	ADD25787	Add25787 Binding d
83	1270.5	47.0	472	6	ABP58289	Abp58289 Humanised
84	1270	47.0	582	4	AAB81987	Aab81987 Gangliosi
85	1270	47.0	619	5	AAU87089	Aau87089 Siglec-BM
86	1269.5	47.0	448	5	ABB99224	Abb99224 Chimeric
87	1269.5	47.0	744	3	AAY94408	Aay94408 Human VCA
88	1268	46.9	634	6	ABB82300	Abb82300 CD19:zeta
89	1267.5	46.9	442	6	ABR39465	Abr39465 Humanised
90	1267.5	46.9	442	6	ABU08311	Abu08311 Humanised
91	1267.5	46.9	442	6	ABB80109	Abb80109 Heavy cha
92	1266	46.9	470	5	ABB81109	Abb81109 Anti-tiss
93	1266	46.9	470	6	ABP72748	Abp72748 Anti-tiss
94	1266	46.9	474	5	AAO14065	Aao14065 Heavy cha
95	1266	46.9	474	6	ABU08017	Abu08017 Human mon
96	1266	46.9	500	7	ADD25837	Add25837 Binding d
97	1266	46.9	500	7	ADD25679	Add25679 Binding d
98	1265.5	46.8	454	2	AAR30774	Aar30774 H52H4-160

99	1265.5	46.8	468	2	AAW85689	Aaw85689 D9D10 hea
100	1265.5	46.8	711	2	AAW85692	Aaw85692 MoTAbII f
101	1265	46.8	448	6	ABR55871	Abr55871 Human imm
102	1265	46.8	449	2	AAR43339	Aar43339 Completel
103	1265	46.8	449	2	AAW49816	Aaw49816 Amino aci
104	1265	46.8	453	6	ABP58287	Abp58287 Humanised
105	1265	46.8	462	4	AAY97592	Aay97592 Flt1 rece
106	1265	46.8	462	5	ABP52445	Abp52445 Mutation
107	1265	46.8	466	2	AAR24812	Aar24812 Sequence
108	1265	46.8	470	5	AAE27923	Aae27923 Human C2B
109	1265	46.8	470	6	ABB82832	Abb82832 Antibody
110	1265	46.8	567	4	AAY97597	Aay97597 Flt1 rece
111	1265	46.8	567	5	ABP52442	Abp52442 Flt1(1-3)
112	1265	46.8	698	5	AAU81012	Aau81012 B7-relate
113	1265	46.8	698	6	AAO16237	Aao16237 B7-relate
114	1264.5	46.8	452	2	AAW69316	Aaw69316 Anti-IL-8
115	1264	46.8	449	6	ABP58273	Abp58273 Humanised
116	1264	46.8	451	5	AAB47726	Aab47726 Heavy cha
117	1264	46.8	466	2	AAR40750	Aar40750 Sequence
118	1264	46.8	567	4	AAY97593	Aay97593 Flt1 rece
119	1264	46.8	567	5	ABP52446	Abp52446 Mutation
120	1263.5	46.8	450	4	AAE10517	Aae10517 Humanised
121	1263.5	46.8	450	4	AAE10509	Aae10509 Humanised
122	1263.5	46.8	450	5	ABP66608	Abp66608 Human RSV
123	1263.5	46.8	450	5	ABP66590	Abp66590 Human RSV
124	1263.5	46.8	450	5	ABP66610	Abp66610 Human RSV
125	1263.5	46.8	450	5	ABP66588	Abp66588 Human RSV

ALIGNMENTS

RESULT 1
AAR26530
ID AAR26530 standard; protein; 435 AA.
XX
AC AAR26530;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1993 (first entry)
XX
DE Sequence of one chain of a CD4-gamma 1 chimeric heavy chain homodimer.
XX
KW CD4-gamma 1 chimeric heavy chaim homodimer; expression vector; HIV;
KW therapy; diagnostic agent; inhibition.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .204
FT /label= CD4
FT /note= "1. .25 = preregion"
FT Region 205. .219
FT /label= hinge
FT Region 220. .329
FT /label= CH2
FT Region 330. .436
FT /label= CH3
XX
PN WO9213559-A1.
XX
PD 20-AUG-1992.
XX
PF 10-FEB-1992; 92WO-US001152.
XX
PR 08-FEB-1991; 91US-00654205.
XX
PA (PROG-) PROGENICS PHARM INC.
XX
PI Beaudry GA, Maddon PJ;
XX
DR WPI; 1992-299758/36.
DR N-PSDB; AAQ27830.
XX
PT CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -
PT for preventing and treating HIV infection useful as a diagnostic agent.
XX
PS Example; Fig 3; 88pp; English.
XX
CC Human CD4 cDNA was excised from pSP6T4 and cloned into M13mp18. The 2 kb
CC PstI/PstI fragment from pBR lambda 1 contg. the human lambda 1 heavy
CC chain gene (contg. the hinge, Ch2 and CH3 exons) was isolated and cloned
CC into the BAP-treated M13mp18/CD4 vector. To obtain a CD4-lambda 1
CC chimeric heavy chain gene, oligonucleotide-mediated site-directed
CC mutagenesis was performed to juxtapose the CD4 and lambda 1 heavy chain
CC DNA sequences, ligating the CD4 sequence in frame to the hinge exon. The
CC DNA was then cloned into pcDNA-1 to produce CD4-IgG1-pcDNA1 (ATCC 40951).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 435 AA;

Query Match 82.0%; Score 2216; DB 2; Length 435;
Best Local Similarity 97.7%; Pred. No. 3.9e-115;
Matches 425; Conservative 0; Mismatches 4; Indels 6; Gaps 2;

```
Qy          2 NRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db          1 NRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 60

Qy         62 LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL 120

Qy        122 VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT 180

Qy        182 WTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTL 236
              |||||||||||||||||   | ||||||||||     ||||||||||||||||||||
Db        181 WTCTVLQNQKKVEFKIDIVVL-AFEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL 239

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 299

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 359

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 419

Qy        417 LHNHYTQKSLSLSPG 431
              |||||||||||||||
Db        420 LHNHYTQKSLSLSPG 434
```

RESULT 2
AAE37574
ID AAE37574 standard; protein; 450 AA.
XX
AC AAE37574;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human D1D2-Ig alphatp fusion protein.
XX
KW Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;
KW human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D1;
KW D2; alpha tailpiece; alphatp; fusion protein.
XX
OS Homo sapiens.
XX
PN WO2003040311-A2.
XX

```
PD   15-MAY-2003.
XX
PF   24-OCT-2002; 2002WO-US034393.
XX
PR   25-OCT-2001; 2001US-0346231P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Arthos J,  Cicala C,  Fauci AS;
XX
DR   WPI; 2003-441545/41.
DR   N-PSDB; AAD29113.
XX
PT   New CD4 polypeptide ligated at its C-terminus with a portion of an
PT   immunoglobulin, useful for preparing a composition for treating or
PT   preventing HIV-1 infection.
XX
PS   Example 1; Page 47; 100pp; English.
XX
CC   The invention relates to a CD4 (cluster of differentiation factor 4)
CC   polypeptide ligated at its C-terminus with a portion of an immunoglobulin
CC   (Ig) comprising a hinge region and a constant domain of a mammalian Ig
CC   heavy chain. The polypeptide comprises a tailpiece from the C-terminus of
CC   the heavy chain of an IgA or IgM antibody. Polypeptides of the invention
CC   are useful for preparing a composition for treating or preventing human
CC   immunodeficiency virus (HIV)-1 infection. The invention is useful in gene
CC   therapy and also in the preparation of vaccines. The present sequence is
CC   a fusion protein which comprises a human IgA alpha tailpiece (alphatp), a
CC   human IgG constant region comprising a hinge, a CH2 and CH3 region and a
CC   human CD4 D1D2 domain
XX
SQ   Sequence 450 AA;

  Query Match             81.0%;  Score 2188.5;  DB 6;  Length 450;
  Best Local Similarity   93.2%;  Pred. No. 1.4e-113;
  Matches  423;  Conservative    2;  Mismatches    8;  Indels   21;  Gaps    3;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDT 235
              |||||||||||||||||||        | ||||||     ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVL-----ASADKTHTCPPCPAPELLGGPSVFLFPPKPKDT 235

Qy        236 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 295

Qy        296 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 355

Qy        356 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415

Qy        416 ALHNHYTQKSLSLSPG-----------LQLDETC 438
              |||||||||||||| |            ::| ||
Db        416 ALHNHYTQKSLSLSAGKPTHVNVSVVMAEVDGTC 449


RESULT 3
AAR26531
ID   AAR26531 standard; protein; 534 AA.
XX
AC   AAR26531;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1993  (first entry)
XX
DE   Sequence of CD4-IgG1 chimeric heavy chain heterotetramer.
XX
KW   CD4-gamma 1 chimeric heavy chaim homodimer; expression vector; HIV;
KW   therapy; diagnostic agent; inhibition.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          205. .302
FT                   /label= CH1
FT   Region          303. .317
FT                   /label= hinge
FT   Region          318. .427
FT                   /label= CH2
FT   Region          428. .534
FT                   /label= CH3
XX
PN   WO9213559-A1.
XX
PD   20-AUG-1992.
XX
PF   10-FEB-1992;   92WO-US001152.
XX
PR   08-FEB-1991;   91US-00654205.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Beaudry GA,  Maddon PJ;
XX
DR   WPI; 1992-299758/36.
DR   N-PSDB; AAQ27831.
XX
PT   CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -
PT   for preventing and treating HIV infection useful as a diagnostic agent.
XX
PS   Example; Fig 4; 88pp; English.
XX
CC   The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into
CC   M13mp18. In order to excise a fragment containing the CH1 exon of the
CC   human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with
CC   SacII, and the SacII sites are then made flush using T4 DNA polymerase.
CC   The fragment containing the CH1 exon is then purified and ligated to the
CC   M13mp18(CD4) vector. Oligonucleotide-mediated site-directed mutagenesis
CC   is then performed to juxtapose the CD4 and CH1 sequences in frame. The
CC   CD4-CH1 chimeric gene is then linearized and ligated to the Pst1-Pst1 DNA
CC   fragment of the plasmid pBr gamma 1 containing the hinge, CH2, and CH3
CC   exons of the human gamma 1 chain gene designated CD4-IgG1HC-pRcCMV (ATCC
CC   75192). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 534 AA;

  Query Match             80.5%;  Score 2176;  DB 2;  Length 534;
  Best Local Similarity   80.3%;  Pred. No. 8.1e-113;
  Matches  428;  Conservative    0;  Mismatches    3;  Indels  102;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
```

```
Qy        181 TWTCTVLQNQKKVEFKIDIV----------------------------PC------PAP 205
              ||||||||||||||||||||                            |       | |
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP 240

Qy        206 ------------------------------------------------------------ 205

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK 300

Qy        206 --EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 258
                ||||||||||      ||||||||||||||||||||||||||||||||||||||||||
Db        301 KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 360

Qy        259 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 420

Qy        319 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 480

Qy        379 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 533
```

RESULT 4
AAE37576
ID AAE37576 standard; protein; 449 AA.
XX
AC AAE37576;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human FD1D2-Ig alphatp fusion protein variant.
XX
KW Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;
KW human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D1;
KW D2; alpha tailpiece; alphatp; fusion protein; mutein; variant; mutant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 218
FT /note= "Wild type Glu substituted with Pro"
FT Misc-difference 219
FT /note= "Wild type Leu substituted with Val"
FT Misc-difference 221
FT /note= "Wild type Gly substituted with Ala"
XX
PN WO2003040311-A2.
XX
PD 15-MAY-2003.
XX
PF 24-OCT-2002; 2002WO-US034393.
XX
PR 25-OCT-2001; 2001US-0346231P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Arthos J, Cicala C, Fauci AS;
XX
DR WPI; 2003-441545/41.
DR N-PSDB; ACC82877.
XX
PT New CD4 polypeptide ligated at its C-terminus with a portion of an
PT immunoglobulin, useful for preparing a composition for treating or
PT preventing HIV-1 infection.
XX
PS Example 11; Page 67; 100pp; English.
XX
CC The invention relates to a CD4 (cluster of differentiation factor 4)
CC polypeptide ligated at its C-terminus with a portion of an immunoglobulin
CC (Ig) comprising a hinge region and a constant domain of a mammalian Ig
CC heavy chain. The polypeptide comprises a tailpiece from the C-terminus of
CC the heavy chain of an IgA or IgM antibody. Polypeptides of the invention
CC are useful for preparing a composition for treating or preventing human
CC immunodeficiency virus (HIV)-1 infection. The invention is useful in gene
CC therapy and also in the preparation of vaccines. The present sequence is
CC a fusion protein variant (G218P/L219V/220delA/G221A) which comprises a
CC human IgA alpha tailpiece (alphatp), a human IgG2 constant region
CC comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain.
CC This variant protein is also referred to as mutant F
XX
SQ Sequence 449 AA;

```
  Query Match             80.3%;  Score 2169;  DB 6;  Length 449;
  Best Local Similarity   92.5%;  Pred. No. 1.6e-112;
  Matches  419;  Conservative    3;  Mismatches   11;  Indels   20;  Gaps    3;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL----LGGPSVFLFPPKPKDTL 236
              |||||||||||||||||||        | |||||||      : ||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVL-----ASADKTHTCPPCPAPPVAGPSVFLFPPKPKDTL 235

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 295

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 355

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 415

Qy        417 LHNHYTQKSLSLSPG-----------LQLDETC 438
              ||||||||||||| |             ::| ||
Db        416 LHNHYTQKSLSLSAGKPTHVNVSVVMAEVDGTC 448
```

RESULT 5
AAP93009
ID AAP93009 standard; protein; 631 AA.
XX
AC AAP93009;
XX
DT 25-MAR-2003 (revised)
DT 02-NOV-1992 (first entry)
XX
DE Genetic construct which encodes CD4 linked to human IgG1 at the Esp site
DE upstream of the hinge region (fusion protein CD4E-gamma-1).
XX
KW Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
KW diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
OS Homo sapiens.
XX
PN EP325262-A.
XX
PD 26-JUL-1989.
XX
PF 20-JAN-1989; 89EP-00100913.
XX
PR 22-JAN-1988; 88US-00147351.

```
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 1989-214472/30.
DR   N-PSDB; AAN90357.
XX
PT   Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
PT   infections or detecting HIV or SIV in sample.
XX
PS   Example; Table 2, Page 24-33; 68pp; English.
XX
CC   The fusion protein genes of the invention pref. comprise cDNA sequences
CC   which encode CD4 or a fragment which binds gp120 ligated to an expression
CC   plasmid which encodes an antibody in which the variable region of the
CC   gene has been deleted (see WO87-02671). The CD4 portion of the fusion
CC   protein may comprise the complete CD4 sequence, the 370 AA extracellular
CC   region and the membrane spanning domain, or the extracellular region. The
CC   Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
CC   specifically claimed: fusion proteins CD4H-gamma-1,CD4Mmu,CD4Pmu,CD4E-
CC   gamma1,and CD4Mmu (No.67608),pCD4P-gamma (No.67609) and pCD4E-gamma-1
CC   (No.67610). The plasmid containing (pCD4E-gamma-1) has been deposited in
CC   E. coli (MC1061/P3) at the ATCC under accession number 67610. (Updated on
CC   25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 631 AA;

  Query Match             78.7%;  Score 2126.5;  DB 1;  Length 631;
  Best Local Similarity   67.8%;  Pred. No. 5.4e-110;
  Matches  427;  Conservative    0;  Mismatches    4;  Indels  199;  Gaps    3;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 -----------------------------------------PCPAP----------- 205
                                                        |   |
Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        206 ------------------------------------------------------------ 205

Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        206 ---------------------------------------EPKSCDKTHTC-----PELLG 221
                                                    ||||||||||     |||||
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG 420

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 480

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 540

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 600

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||
Db        601 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 630


RESULT 6
AAB19508
ID   AAB19508 standard; protein; 631 AA.
XX
AC   AAB19508;
XX
DT   09-JAN-2001  (first entry)
XX
DE   CD4-IgG1 fusion protein CH4Egamma1.
XX
KW   CD4; IgG1; human; CD4Egamma1; fusion protein; immunoglobulin; HIV; SIV;
KW   gp120; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .395
FT                   /note= "CD4 extracellular region"
FT   Protein         400. .631
FT                   /note= "IgG1 heavy chain"
XX
PN   US6117656-A.
XX
PD   12-SEP-2000.
XX
PF   07-JUN-1995;   95US-00479353.
XX
PR   22-JAN-1988;   88US-00147351.
PR   23-JAN-1989;   89US-00299596.
PR   09-JUN-1992;   92US-00896781.
PR   12-APR-1993;   93US-00057952.
PR   04-FEB-1994;   94US-00191708.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-586558/55.
DR   N-PSDB; AAA50661.
XX
PT   CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
PT   SIV.
XX
PS   Example 1; Col 29-42; 39pp; English.
XX
CC   The present sequence is that of fusion protein CD4Egamma1 comprising the
CC   extracellular portion of CD4, which binds to HIV gp120, linked at its C-
CC   terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
CC   encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge
CC   region (see AAA50661). Fusion protein CD4Egamma1 and a nucleic acid
CC   encoding it are claimed. Also claimed are a vector comprising the nucleic
CC   acid, and a method of producing the fusion protein in secreted form using
CC   a transformed host cell. The fusion protein may further comprise a
CC   therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
CC   can be administered to an animal (including humans) for treatment of HIV
CC   or SIV infection, and can also be used in assays for HIV or SIV, imaging
CC   and tissue stains. IgG1 fusion proteins such as CD4Egamma1 provide both
CC   complement-mediated and cell-mediated immunity
XX
SQ   Sequence 631 AA;

  Query Match             78.7%;  Score 2126.5;  DB 3;  Length 631;
  Best Local Similarity   67.8%;  Pred. No. 5.4e-110;
  Matches  427;  Conservative    0;  Mismatches    4;  Indels  199;  Gaps    3;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
```

```
Qy          61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy         181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
               ||||||||||||||||||||
Db         181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy         201 -------------------------------------------PCPAP----------- 205
                                                          |   |
Db         241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy         206 ------------------------------------------------------------ 205

Db         301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy         206 ---------------------------------------EPKSCDKTHTC-----PELLG 221
                                                     ||||||||||     |||||
Db         361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG 420

Qy         222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 480

Qy         282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 540

Qy         342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 600

Qy         402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               |||||||||||||||||||||||||||||
Db         601 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 630
```

```
RESULT 7
AAY51079
ID   AAY51079 standard; protein; 631 AA.
XX
AC   AAY51079;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Human fusion protein CD4Egamma1.
XX
KW   Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
KW   anti-human immunodeficiency virus; CD4Egamma1.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6004781-A.
XX
PD   21-DEC-1999.
XX
PF   04-FEB-1994;   94US-00191708.
XX
PR   22-JAN-1988;   88US-00147351.
PR   23-JAN-1989;   89US-00299596.
PR   09-JUN-1992;   92US-00896781.
PR   12-APR-1993;   93US-00057952.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-085792/07.
DR   N-PSDB; AAZ44062.
XX
PT   Fusion protein useful for the treatment of human immunodeficiency virus.
XX
PS   Example 1; Col 29-42; 39pp; English.
XX
CC   This invention describes a novel nucleic acid (I) encoding a fusion
CC   protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
CC   and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC   chain (III). The products pf the invention have anti-human
CC   immunodeficiency virus (HIV) activity and are capable of binding to
CC   gp120. The fusion protein is useful for treating human immunodeficiency
CC   virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC   represents the fusion protein CD4Egamma1 which is constructed from CD4
CC   linked to human IgG1 upstream of the hinge region
XX
SQ   Sequence 631 AA;

  Query Match           78.7%;  Score 2126.5;  DB 3;  Length 631;
  Best Local Similarity   67.8%;  Pred. No. 5.4e-110;
  Matches  427;  Conservative    0;  Mismatches    4;  Indels  199;  Gaps    3;

Qy           1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db           1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy          61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy         181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
               ||||||||||||||||||||
Db         181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy         201 -------------------------------------------PCPAP----------- 205
                                                          |   |
Db         241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy         206 ------------------------------------------------------------ 205

Db         301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy         206 ---------------------------------------EPKSCDKTHTC-----PELLG 221
                                                     ||||||||||     |||||
Db         361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG 420

Qy         222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 480

Qy         282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 540

Qy         342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 600

Qy         402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               |||||||||||||||||||||||||||||
Db         601 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 630
```

```
RESULT 8
AAY59169
ID   AAY59169 standard; protein; 631 AA.
XX
AC   AAY59169;
XX
```

```
DT   14-MAR-2000  (first entry)
XX
DE   CD4-Ig fusion protein CD4Egamma1.
XX
KW   HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
KW   secreted protein; SIV infection; medicament.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   CA1340741-C.
XX
PD   14-SEP-1999.
XX
PF   20-JAN-1989;   89CA-00588749.
XX
PR   20-JAN-1989;   89CA-00588749.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-063015/06.
DR   N-PSDB; AAZ48202.
XX
PT   New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
PT   the treatment of HIV or simian immunodeficiency virus infections.
XX
PS   Example 1; Page 37-46; 89pp; English.
XX
CC   The invention provides a fusion gene encoding a fusion protein that
CC   comprises an extracellular CD4 DNA sequence or its fragment which binds
CC   to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
CC   sequence of an Ig heavy or light chain, where the DNA sequence encoding
CC   the variable region has been replaced with the DNA sequence which encodes
CC   extracellular CD4 or its gp120 binding fragment. The fusion protein is
CC   capable of being secreted. The fusion proteins are useful for treating
CC   HIV or SIV infections in animals, preferably humans. They are also useful
CC   for producing medicaments which can be used for treating HIV or SIV
CC   infections in humans. The present sequence represents the fusion protein
CC   CD4Egamma1 where the CD4 is linked to human IgG1 at the Esp site upstream
CC   of the hinge region
XX
SQ   Sequence 631 AA;

  Query Match            78.7%;  Score 2126.5;  DB 3;  Length 631;
  Best Local Similarity  67.8%;  Pred. No. 5.4e-110;
  Matches  427;  Conservative    0;  Mismatches    4;  Indels  199;  Gaps    3;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 -------------------------------------------PCPAP----------- 205
                                                          |   |
Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        206 ------------------------------------------------------------ 205

Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        206 -----------------------------------EPKSCDKTHTC-----PELLG 221
                                                  ||||||||||     |||||
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG 420

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 480

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 540

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 600

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||
Db        601 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 630


RESULT 9
AAR26782
ID   AAR26782 standard; protein; 432 AA.
XX
AC   AAR26782;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   06-FEB-1993  (first entry)
XX
DE   CD4-gamma2 chimeric heavy chain homodimer.
XX
KW   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW   chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .216
FT                   /label= CD4
FT   Domain          217. .325
FT                   /label= CH2
FT   Domain          326. .433
FT                   /label= CH3
XX
PN   WO9213947-A1.
XX
PD   20-AUG-1992.
XX
PF   10-FEB-1992;   92WO-US001143.
XX
PR   08-FEB-1991;   91US-00653684.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Beaudry GA,  Maddon PJ;
XX
DR   WPI; 1992-300034/36.
DR   N-PSDB; AAQ28088.
XX
PT   CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT   treatment, prevention and diagnosis of HIV infection.
XX
PS   Claim 2; Fig 3; 90pp; English.
XX
CC   This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It
CC   was produced by expresion of the coding mutagenised cDNA (produced as
CC   described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently
CC   assembled intracellularly and effectively secreted from mammalian cells
CC   pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery
CC   and purification from the medium of cells expressing it. It possesses
```

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CC   increased serum half-life and has increased avidity for HIV cf. heavy
CC   chain dimers. It can inhibit HIV infection of CD4+ cells and block the
CC   spread of HIV infection within a patient. Attachment to a detectable
CC   marker makes it useful in an assay for HIV or SIV infection, and it can
CC   also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domainS
CC   I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003
CC   to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 432 AA;

  Query Match             78.5%;  Score 2122;  DB 2;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 6.4e-110;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV-------------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
              |||||||||||||||||||              |||||              : ||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP-------------VAGPSVFL 227

Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
              ||||||||||||||||||||||||||||:||||||||||||||||||||:|||:||
Db        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287

Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
              ||||||:|||||||||||||||| |||||||||| ||||||||||||||:|:||||
Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||
Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 10
AAR46678
ID   AAR46678 standard; protein; 432 AA.
XX
AC   AAR46678;
XX
DT   25-MAR-2003  (revised)
DT   08-AUG-1994  (first entry)
XX
DE   CD4-gamma 2 chimeric heavy chain.
XX
KW   CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV;
KW   human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
KW   imaging; detection; targetting.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .204
FT                   /label= CD4 Region.
FT   Region          205. .216
FT                   /label= Hinge Region.
FT   Region          217. .325
FT                   /label= CH2 Region.
FT   Region          326. .432
FT                   /label= CH3 Region.
XX
PN   WO9403191-A1.
XX
PD   17-FEB-1994.
XX
PF   06-AUG-1993;   93WO-US007422.
XX
PR   07-AUG-1992;   92US-00927931.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Allaway GP,  Maddon PJ;
XX
DR   WPI; 1994-065392/08.
DR   N-PSDB; AAQ57750.
XX
PT   Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
PT   immuno:conjugates - used to kill HIV-infected cells and to image and
PT   stage HIV infection.
XX
PS   Disclosure; Fig 3; 142pp; English.
XX
CC   A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non- peptidyl
CC   toxin or a gamma radiation-emitting radionuclide of low to moderate
CC   cytotoxicity. The resulting immunoconjugate comprising the toxin can be
CC   used to kill HIV infected cells and to treat HIV infected subjects to
CC   reduce the population of HIV infected cells. It can also be used to
CC   reduce the likelihood of infection. The immunoconjugate comprising the
CC   radionuclide can be used to image HIV infected tissue, to calculate the
CC   stage of HIV infection or the efficacy of an anti-HIV treatment using the
CC   imaging technique and for determining the prognosis of an HIV infected
CC   subject. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 432 AA;

  Query Match             78.5%;  Score 2122;  DB 2;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 6.4e-110;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV-------------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
              |||||||||||||||||||              |||||              : ||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP-------------VAGPSVFL 227

Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
              ||||||||||||||||||||||||||||:||||||||||||||||||||:|||:||
Db        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287

Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
              ||||||:|||||||||||||||| |||||||||| ||||||||||||||:|:||||
Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||
Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 11
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```
AAY85079
ID   AAY85079 standard; protein; 432 AA.
XX
AC   AAY85079;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
XX
KW   CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment;
KW   cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW   cellular immune response interaction mediator; HIV interaction; staging;
KW   prognosis; envelope glycoprotein burden; human.
XX
OS   Homo sapiens.
XX
PN   US6034223-A.
XX
PD   07-MAR-2000.
XX
PF   07-JUN-1995;   95US-00477460.
XX
PR   07-AUG-1992;   92US-00927931.
PR   06-AUG-1993;   93WO-US007422.
PR   03-FEB-1995;   95US-00379516.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Allaway GP,  Maddon PJ;
XX
DR   WPI; 2000-269502/23.
DR   N-PSDB; AAZ98855.
XX
PT   New immunoconjugate, used to treat, prevent or image human immune
PT   deficiency virus infection, comprises radionuclide attached to
PT   heterotetramer of CD4-immunoglobulin chimeras.
XX
PS   Disclosure; Fig 3; 58pp; English.
XX
CC   This sequence represents the human CD4-gamma 2 chimeric heavy chain
CC   homodimer amino acid sequence. The invention relates to an
CC   immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer
CC   of two heavy chains and two light chains. The cytotoxic radionuclide is
CC   linked to either the heavy chains or the light chains, or to all four
CC   chains, directly or through a bifunctional chelator. Both heavy chains
CC   are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-
CC   IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-kappa
CC   chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-
CC   polymorphic cell surface glycoprotein that is expressed on the surface of
CC   helper T lymphocytes, cells of the monocyte/macrophage lineage and
CC   dendritic cells. CD4 associates with major histocompatibility complex
CC   (MHC) class II molecules on the surface of antigen presenting cells to
CC   mediate efficient cellular immune response interactions. In humans CD4 is
CC   the target of interaction with the human immunodeficiency virus HIV. The
CC   immunoconjugate is used to kill cells infected with HIV, and for treating
CC   or preventing infection. It is also used for imaging HIV-infected tissues
CC   (for staging or prognosis of infection, and for assessing efficacy of
CC   treatments). The immunoconjugate is also used to determine the HIV
CC   envelope glycoprotein burden, once determined, this information is used
CC   in the staging and prognosis of HIV infected patients. The
CC   immunoconjugate should be active against all strains of HIV (since the
CC   CD4-gp120 interaction is essential for infection). The heterotetramers
CC   are assembled intracellularly and secreted efficiently from mammalian
CC   cells, allowing high recovery and purification from the culture medium.
CC   They have longer half-life in serum and greater avidity than heavy chain
CC   dimers
XX
SQ   Sequence 432 AA;

  Query Match           78.5%;  Score 2122;  DB 3;  Length 432;
  Best Local Similarity  91.2%;  Pred. No. 6.4e-110;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV------------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
              |||||||||||||||||||              |||||              : ||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP------------VAGPSVFL 227

Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
              ||||||||||||||||||||||||||||:||||||||||||||||||||:|||:||
Db        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287

Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
              ||||||:|||||||||||||| |||||||||| ||||||||||||||:|:||||
Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||
Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 12
AAB67322
ID   AAB67322 standard; protein; 432 AA.
XX
AC   AAB67322;
XX
DT   23-APR-2001  (first entry)
XX
DE   CD4-gamma2 chimeric heavy chain homodimer protien.
XX
KW   Immunoconjugate; chelator; chimeric; HIV; human immunodeficiency virus.
XX
OS   Homo sapiens.
XX
PN   US6177549-B1.
XX
PD   23-JAN-2001.
XX
PF   10-JUN-1999;   99US-00329916.
XX
PR   07-AUG-1992;   92US-00927931.
PR   06-AUG-1993;   93WO-US007422.
PR   03-FEB-1995;   95US-00379516.
PR   07-JUN-1995;   95US-00477460.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Maddon PJ,  Allaway GP;
XX
DR   WPI; 2001-158582/16.
XX
PT   Immunoconjugate for treating human immunodeficiency virus-infected
PT   subject, consists of cytotoxic radionuclide linked to heterotetramer
PT   comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
PT   kappalight chains.
XX
PS   Disclosure; Fig 3; 43pp; English.
XX
CC   The present invention relates to an immunoconjugate, comprising a
CC   cytotoxic radionuclide linked, directly or via a bifunctional chelator,
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CC   to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by
CC   an expression vector CD4-IgG2HC-pRcCMV and two chimeric CD4-kappa light
CC   chains encoded by an expression vector CD4-kLC-pRcMV. The invention is
CC   useful for killing human immunodeficiency virus (HIV)-infected cells, for
CC   the treatment and prevention of infection with HIV
XX
SQ   Sequence 432 AA;

  Query Match             78.5%;  Score 2122;  DB 4;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 6.4e-110;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
              |||||||||||||||||||              |||||              : ||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP----------VAGPSVFL 227

Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
              ||||||||||||||||||||||||||||:||||||||||||||||||||:|||:||
Db        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287

Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
              |||||:|||||||||||||||| |||||||||| |||||||||||||||:|:||||
Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||
Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 13
AAB80883
ID   AAB80883 standard; protein; 432 AA.
XX
AC   AAB80883;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Human CD4-gamma2 chimeric heavy chain homodimer.
XX
KW   Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
KW   immunoglobulin gamma 2.
XX
OS   Homo sapiens.
XX
PN   US6187748-B1.
XX
PD   13-FEB-2001.
XX
PF   07-JUN-1995;   95US-00485372.
XX
PR   08-FEB-1991;   91US-00653684.
PR   10-FEB-1992;   92WO-US001143.
PR   08-DEC-1992;   92US-00960440.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Maddon PJ,  Beaudry GA;
XX
DR   WPI; 2001-264981/27.
DR   N-PSDB; AAF77829.
XX
PT   Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
PT   or treating a subject having CD4+ cells infected with HIV involves using
PT   CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
XX
PS   Disclosure; Fig 3; 55pp; English.
XX
CC   The present invention relates to a method for inhibiting infection of a
CC   CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
CC   chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of
CC   differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface
CC   glycoprotein that is expressed primarily on the surface of T cells. In
CC   man, CD4 is the target of interaction with HIV. The heterotetramer has
CC   two heavy and two light chains which are encoded by expression vectors
CC   CD4-IgG2HC-pRcCMV (V1) and CD4-kLC-pRcCMV (V2), respectively. The method
CC   is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+
CC   cells of a subject from becoming infected with HIV. The method is also
CC   useful for treating a subject having CD4+ cells infected with HIV. The
CC   present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain
CC   homodimer. This sequence was used in the method of the present invention
XX
SQ   Sequence 432 AA;

  Query Match             78.5%;  Score 2122;  DB 4;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 6.4e-110;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
              |||||||||||||||||||              |||||              : ||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP----------VAGPSVFL 227

Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
              ||||||||||||||||||||||||||||:||||||||||||||||||||:|||:||
Db        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287

Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
              |||||:|||||||||||||||| |||||||||| |||||||||||||||:|:||||
Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||
Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 14
ABG71122
ID   ABG71122 standard; protein; 432 AA.
XX
AC   ABG71122;
XX
DT   17-JAN-2003  (first entry)
XX
DE   CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric protein.
XX
```

```
KW   CD4; gamma2 heavy chain; human immunodeficiency virus-1; HIV-1; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal_peptide
FT   Protein         26. .432
FT                   /note= "Mature CD4-gamma2 chimeric heavy chain of the CD4
FT                   -IgG2 chimeric heterotetramer"
XX
PN   US6451313-B1.
XX
PD   17-SEP-2002.
XX
PF   07-JUN-1995;   95US-00484681.
XX
PR   08-FEB-1991;   91US-00653684.
PR   10-FEB-1992;   92WO-US001143.
PR   08-DEC-1992;   92US-00960440.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Maddon PJ,  Beaudry GA;
XX
DR   WPI; 2003-038273/03.
DR   N-PSDB; ABS55720.
XX
PT   Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human
PT   immunodeficiency virus-1 with two heavy and light chains encoded by
PT   expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
PT   respectively.
XX
PS   Disclosure; Fig 3A-F; 54pp; English.
XX
CC   The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric
CC   heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-
CC   1) having two heavy chains encoded by an expression vector designated CD4
CC   -IgG2HC-pRcCMV, and two light chains encoded by expression vector
CC   designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or
CC   (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4
CC   cell, and preventing a subject being infected with HIV by blocking the
CC   spread of HIV infection. This is the amino acid sequence of the CD4-
CC   gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer
CC   useful in inhibiting HIV infection
XX
SQ   Sequence 432 AA;

  Query Match             78.5%;  Score 2122;  DB 6;  Length 432;
  Best Local Similarity   91.2%;  Pred. No. 6.4e-110;
  Matches  405;  Conservative    8;  Mismatches    5;  Indels   26;  Gaps    2;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------PCPAPEPKSCDKTHTCPELLGGPSVFL 227
              |||||||||||||||||||          |||||              : ||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP----------VAGPSVFL 227

Qy        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 287
              ||||||||||||||||||||||||||:||||||||||||||||||:|||:||
Db        228 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV 287

Qy        288 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ 347
              ||||||:|||||||||||||||| |||||||||| |||||||||||||||:|:||||
Db        288 VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ 347

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV 407

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||
Db        408 FSCSVMHEALHNHYTQKSLSLSPG 431


RESULT 15
AAR26783
ID   AAR26783 standard; protein; 530 AA.
XX
AC   AAR26783;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   06-FEB-1993  (first entry)
XX
DE   CD4-IgG2 chimeric heavy chain.
XX
KW   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW   chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .205
FT                   /label= CD4 domain
FT   Domain          206. .302
FT                   /label= CH1 domain
FT   Domain          303. .312
FT                   /label= hinge domain
FT   Domain          313. .423
FT                   /label= CH2 domain
FT   Domain          424. .530
FT                   /label= CH3 domain
XX
PN   WO9213947-A1.
XX
PD   20-AUG-1992.
XX
PF   10-FEB-1992;   92WO-US001143.
XX
PR   08-FEB-1991;   91US-00653684.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Beaudry GA,  Maddon PJ;
XX
DR   WPI; 1992-300034/36.
DR   N-PSDB; AAQ28089.
XX
PT   CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT   treatment, prevention and diagnosis of HIV infection.
XX
PS   Claim 15; Fig 4; 90pp; English.
XX
CC   This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer
CC   It was produced by expresion of the coding mutagenised cDNA (produced as
CC   described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently
CC   assembled intracellularly and effectively secreted from mammalian cells
CC   pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high
CC   recovery and purification from the medium of cells expressing it. It
CC   possesses increased serum half-life and has increased avidity for HIV cf.
CC   heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block
CC   the spread of HIV infection within a patient. Attachment to a detectable
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CC   marker makes it useful in an assay for HIV or SIV infection, and it can
CC   also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domainS
CC   I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003
CC   to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 530 AA;

  Query Match             77.2%;  Score 2085;  DB 2;  Length 530;
  Best Local Similarity   77.3%;  Pred. No. 8.9e-108;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              ||||||||||||||||||||                ||                |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : ||||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              |||||||||||||||||:|||:||||||||:|||||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 16
AAY85080
ID   AAY85080 standard; protein; 530 AA.
XX
AC   AAY85080;
XX
DT   19-JUN-2000  (first entry)
XX
DE   CD4-IgG2 chimeric heterotetramer heavy chain amino acid sequence.
XX
KW   CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment;
KW   cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW   cellular immune response interaction mediator; HIV interaction; staging;
KW   prognosis; envelope glycoprotein burden; human.
XX
OS   Homo sapiens.
XX
PN   US6034223-A.
XX
PD   07-MAR-2000.
XX
PF   07-JUN-1995;   95US-00477460.
XX
PR   07-AUG-1992;   92US-00927931.
PR   06-AUG-1993;   93WO-US007422.
PR   03-FEB-1995;   95US-00379516.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Allaway GP,  Maddon PJ;
XX
DR   WPI; 2000-269502/23.
DR   N-PSDB; AAZ98856.
XX
PT   New immunoconjugate, used to treat, prevent or image human immune
PT   deficiency virus infection, comprises radionuclide attached to
PT   heterotetramer of CD4-immunoglobulin chimeras.
XX
PS   Disclosure; Fig 4; 58pp; English.
XX
CC   This sequence represents the CD4-IgG2 chimeric heavy chain amino acid
CC   sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates
CC   to an immunoconjugate comprising a cytotoxic radionuclide and a
CC   heterotetramer of two heavy chains and two light chains. The cytotoxic
CC   radionuclide is linked to either the heavy chains or the light chains, or
CC   to all four chains, directly or through a bifunctional chelator. Both
CC   heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by
CC   vector CD4-IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric
CC   CD4-kappa chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a
CC   non-polymorphic cell surface glycoprotein that is expressed on the
CC   surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
CC   and dendritic cells. CD4 associates with major histocompatibility complex
CC   (MHC) class II molecules on the surface of antigen presenting cells to
CC   mediate efficient cellular immune response interactions. In humans CD4 is
CC   the target of interaction with the human immunodeficiency virus HIV. The
CC   immunoconjugate is used to kill cells infected with HIV, and for treating
CC   or preventing infection. It is also used for imaging HIV-infected tissues
CC   (for staging or prognosis of infection, and for assessing efficacy of
CC   treatments). The immunoconjugate is also used to determine the HIV
CC   envelope glycoprotein burden, once determined, this information is used
CC   in the staging and prognosis of HIV infected patients. The
CC   immunoconjugate should be active against all strains of HIV (since the
CC   CD4-gp120 interaction is essential for infection). The heterotetramers
CC   are assembled intracellularly and secreted efficiently from mammalian
CC   cells, allowing high recovery and purification from the culture medium.
CC   They have longer half-life in serum and greater avidity than heavy chain
CC   dimers
XX
SQ   Sequence 530 AA;

  Query Match             77.2%;  Score 2085;  DB 3;  Length 530;
  Best Local Similarity   77.3%;  Pred. No. 8.9e-108;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              ||||||||||||||||||||                ||                |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : ||||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360
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```
Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||||:|||:||||||||:||||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 17
AAB67323
ID   AAB67323 standard; protein; 530 AA.
XX
AC   AAB67323;
XX
DT   23-APR-2001  (first entry)
XX
DE   CD4-IgG2 chimeric heavy chain protein.
XX
KW   Immunoconjugate; chelator; chimeric; HIV; human immunodeficiency virus.
XX
OS   Homo sapiens.
XX
PN   US6177549-B1.
XX
PD   23-JAN-2001.
XX
PF   10-JUN-1999;   99US-00329916.
XX
PR   07-AUG-1992;   92US-00927931.
PR   06-AUG-1993;   93WO-US007422.
PR   03-FEB-1995;   95US-00379516.
PR   07-JUN-1995;   95US-00477460.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Maddon PJ,. Allaway GP;
XX
DR   WPI; 2001-158582/16.
XX
PT   Immunoconjugate for treating human immunodeficiency virus-infected
PT   subject, consists of cytotoxic radionuclide linked to heterotetramer
PT   comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
PT   kappalight chains.
XX
PS   Disclosure; Fig 4; 43pp; English.
XX
CC   The present invention relates to an immunoconjugate, comprising a
CC   cytotoxic radionuclide linked, directly or via a bifunctional chelator,
CC   to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by
CC   an expression vector CD4-IgG2HC-pRcCMV and two chimeric CD4-kappa light
CC   chains encoded by an expression vector CD4-kLC-pRcMV. The invention is
CC   useful for killing human immunodeficiency virus (HIV)-infected cells, for
CC   the treatment and prevention of infection with HIV
XX
SQ   Sequence 530 AA;

  Query Match             77.2%;  Score 2085;  DB 4;  Length 530;
  Best Local Similarity   77.3%;  Pred. No. 8.9e-108;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              ||||||||||||||||||||                ||                |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : ||||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||:|||:||||||||:||||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 18
AAB80884
ID   AAB80884 standard; protein; 530 AA.
XX
AC   AAB80884;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Human CD4-IgG2 chimeric heavy chain.
XX
KW   Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
KW   immunoglobulin gamma 2.
XX
OS   Homo sapiens.
XX
PN   US6187748-B1.
XX
PD   13-FEB-2001.
XX
PF   07-JUN-1995;   95US-00485372.
XX
PR   08-FEB-1991;   91US-00653684.
PR   10-FEB-1992;   92WO-US001143.
PR   08-DEC-1992;   92US-00960440.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Maddon PJ,  Beaudry GA;
XX
DR   WPI; 2001-264981/27.
DR   N-PSDB; AAF77830.
XX
PT   Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
PT   or treating a subject having CD4+ cells infected with HIV involves using
PT   CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
XX
PS   Disclosure; Fig 4; 55pp; English.
XX
CC   The present invention relates to a method for inhibiting infection of a
CC   CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
CC   chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of
CC   differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface
CC   glycoprotein that is expressed primarily on the surface of T cells. In
CC   man, CD4 is the target of interaction with HIV. The heterotetramer has
```

```
CC   two heavy and two light chains which are encoded by expression vectors
CC   CD4-IgG2HC-pRcCMV (V1) and CD4-kLC-pRcCMV (V2), respectively. The method
CC   is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+
CC   cells of a subject from becoming infected with HIV. The method is also
CC   useful for treating a subject having CD4+ cells infected with HIV. The
CC   present sequence is human fusion protein: CD4-Ig2 chimeric heavy chain of
CC   the CD4-IgG2 chimeric heterotetramer. This sequence was used in the
CC   method of the present invention
XX
SQ   Sequence 530 AA;

  Query Match             77.2%;  Score 2085;  DB 4;  Length 530;
  Best Local Similarity   77.3%;  Pred. No. 8.9e-108;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              |||||||||||||||||||                ||                |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : |||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||:|||:|||||||:|||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | |||||||||||||||:|:||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 19
ABG71123
ID   ABG71123 standard; protein; 530 AA.
XX
AC   ABG71123;
XX
DT   17-JAN-2003  (first entry)
XX
DE   CD4-immunoglobulin G2 (IgG2) chimeric heterotetramer.
XX
KW   CD4; immunoglobulin G2; Ig gamma2; human immunodeficiency virus-1; HIV-1;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal_peptide
FT   Protein         26. .530
FT                   /note= "Mature CD4-IgG2 chimeric heterotetramer"
XX
PN   US6451313-B1.
XX
PD   17-SEP-2002.
XX
PF   07-JUN-1995;   95US-00484681.
XX
PR   08-FEB-1991;   91US-00653684.
PR   10-FEB-1992;   92WO-US001143.
PR   08-DEC-1992;   92US-00960440.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Maddon PJ,  Beaudry GA;
XX
DR   WPI; 2003-038273/03.
DR   N-PSDB; ABS55721.
XX
PT   Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human
PT   immunodeficiency virus-1 with two heavy and light chains encoded by
PT   expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
PT   respectively.
XX
PS   Claim 1; Fig 4A-H; 54pp; English.
XX
CC   The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric
CC   heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-
CC   1) having two heavy chains encoded by an expression vector designated CD4
CC   -IgG2HC-pRcCMV, and two light chains encoded by expression vector
CC   designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or
CC   (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4
CC   cell, and preventing a subject being infected with HIV by blocking the
CC   spread of HIV infection. This is the amino acid sequence of the CD4-
CC   immunoglobulin G2 chimeric heavy chain chimeric heterotetramer useful in
CC   inhibiting HIV infection
XX
SQ   Sequence 530 AA;

  Query Match             77.2%;  Score 2085;  DB 6;  Length 530;
  Best Local Similarity   77.3%;  Pred. No. 8.9e-108;
  Matches  409;  Conservative    9;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              |||||||||||||||||||                ||                |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : |||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              ||||||||||||||||:|||:|||||||:|||||||||||||| ||||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | |||||||||||||||:|:||||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480
```

```
Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529
```

RESULT 20
AAY51082
ID AAY51082 standard; protein; 616 AA.
XX
AC AAY51082;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human fusion protein CD4Bgamma1.
XX
KW Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
KW anti-human immunodeficiency virus; CD4Bgamma1.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6004781-A.
XX
PD 21-DEC-1999.
XX
PF 04-FEB-1994; 94US-00191708.
XX
PR 22-JAN-1988; 88US-00147351.
PR 23-JAN-1989; 89US-00299596.
PR 09-JUN-1992; 92US-00896781.
PR 12-APR-1993; 93US-00057952.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 2000-085792/07.
DR N-PSDB; AAZ44065.
XX
PT Fusion protein useful for the treatment of human immunodeficiency virus.
XX
PS Example 1; Col 59-70; 39pp; English.
XX
CC This invention describes a novel nucleic acid (I) encoding a fusion
CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC chain (III). The products pf the invention have anti-human
CC immunodeficiency virus (HIV) activity and are capable of binding to
CC gp120. The fusion protein is useful for treating human immunodeficiency
CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC represents the fusion protein CD4Egamma1 which is constructed from CD4
CC linked to human IgG1 upstream of the hinge region
XX
SQ Sequence 616 AA;

Query Match 77.0%; Score 2081; DB 3; Length 616;
Best Local Similarity 68.1%; Pred. No. 1.8e-107;
Matches 419; Conservative 1; Mismatches 11; Indels 184; Gaps 3;

```
Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 ----------------------------------------------PCPAPE---------- 206
                                                           |   |:
Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        207 ------------------PKSCDKTHTC------------------------------ 216
                               |   ||
Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        217 ---------------------------------------PELLGGPSVFLFPPKPKDTL 236
                                                      ||||||||||||||||||||
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL 420

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 480

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 540

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 600

Qy        417 LHNHYTQKSLSLSPG 431
              |||||||||||||||
Db        601 LHNHYTQKSLSLSPG 615
```

RESULT 21
AAY59172
ID AAY59172 standard; protein; 616 AA.
XX
AC AAY59172;
XX
DT 14-MAR-2000 (first entry)
XX
DE CD4-Ig fusion protein CD4Bgamma1.
XX
KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
KW secreted protein; SIV infection; medicament.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CA1340741-C.
XX
PD 14-SEP-1999.
XX
PF 20-JAN-1989; 89CA-00588749.
XX
PR 20-JAN-1989; 89CA-00588749.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 2000-063015/06.
DR N-PSDB; AAZ48205.
XX
PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
PT the treatment of HIV or simian immunodeficiency virus infections.
XX
PS Example 1; Page 61-68; 89pp; English.
XX
CC The invention provides a fusion gene encoding a fusion protein that
CC comprises an extracellular CD4 DNA sequence or its fragment which binds
CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
CC sequence of an Ig heavy or light chain, where the DNA sequence encoding
CC the variable region has been replaced with the DNA sequence which encodes

```
CC   extracellular CD4 or its gp120 binding fragment. The fusion protein is
CC   capable of being secreted. The fusion proteins are useful for treating
CC   HIV or SIV infections in animals, preferably humans. They are also useful
CC   for producing medicaments which can be used for treating HIV or SIV
CC   infections in humans. The present sequence represents the fusion protein
CC   CD4Bgamma1 where the CD4 is linked to human IgG1 at the Ban1 site
CC   downstream from the hinge region
XX
SQ   Sequence 616 AA;

  Query Match             77.0%;  Score 2081;  DB 3;  Length 616;
  Best Local Similarity   68.1%;  Pred. No. 1.8e-107;
  Matches  419;  Conservative    1;  Mismatches   11;  Indels  184;  Gaps    3;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 ----------------------------------------------PCPAPE---------- 206
                                                           |   |:
Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        207 ------------------PKSCDKTHTC------------------------------ 216
                               |  ||
Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        217 ---------------------------------------PELLGGPSVFLFPPKPKDTL 236
                                                     ||||||||||||||||||||
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL 420

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 480

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 540

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 600

Qy        417 LHNHYTQKSLSLSPG 431
              |||||||||||||||
Db        601 LHNHYTQKSLSLSPG 615


RESULT 22
AAP93008
ID   AAP93008 standard; protein; 729 AA.
XX
AC   AAP93008;
XX
DT   25-MAR-2003  (revised)
DT   02-NOV-1992  (first entry)
XX
DE   Genetic construct which encodes CD4 linked to human IgG1 at the Hind3
DE   site upstream of the CH1 region (fusion protein CD4H-gamma-1).
XX
KW   Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
KW   diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
OS   Homo sapiens.
XX
PN   EP325262-A.
XX
PD   26-JUL-1989.
XX
PF   20-JAN-1989;   89EP-00100913.
XX
PR   22-JAN-1988;   88US-00147351.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 1989-214472/30.
DR   N-PSDB; AAN90356.
XX
PT   Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
PT   infections or detecting HIV or SIV in sample.
XX
PS   Example; Table 1, Page 12-23; 68pp; English.
XX
CC   The fusion protein genes of the invention pref. comprise cDNA sequences
CC   which encode CD4 or a fragment which binds gp120 ligated to an expression
CC   plasmid which encodes an antibody in which the variable region of the
CC   gene has been deleted (see WO87-02671). The CD4 portion of the fusion
CC   protein may comprise the complete CD4 sequence, the 370 AA extracellular
CC   region and the membrane spanning domain, or the extracellular region. The
CC   Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
CC   specifically claimed: fusion proteins CD4H-gamma-1,CD4Mmu,CD4Pmu,CD4E-
CC   gamma1,and CD4Mmu (No.67608),pCD4P-gamma (No.67609) and pCD4E-gamma-1
CC   (No.67610). The plasmid containing (pCD4H-gamma-1) has been deposited in
CC   E. coli (MC1061/P3) at the ATCC under accession number 67611. (Updated on
CC   25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 729 AA;

  Query Match             77.0%;  Score 2079.5;  DB 1;  Length 729;
  Best Local Similarity   58.8%;  Pred. No. 2.5e-107;
  Matches  428;  Conservative    0;  Mismatches    3;  Indels  297;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 ---------------------------------------------------------- 200

Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        201 ---------------------------------------------------------- 200

Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        201 --------PC---------------------------------------------------- 202
                      |
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG 420

Qy        203 ------------PAP------------------------------------------- 205
                         | |
Db        421 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY 480
```

```
Qy        206 -----------------EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE 243
                               ||||||||||      ||||||||||||||||||||||||||||
Db        481 ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 540

Qy        244 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 600

Qy        304 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 660

Qy        364 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 720

Qy        424 KSLSLSPG 431
              ||||||||
Db        721 KSLSLSPG 728
```

```
RESULT 23
AAB19507
ID   AAB19507 standard; protein; 729 AA.
XX
AC   AAB19507;
XX
DT   09-JAN-2001  (first entry)
XX
DE   CD4-IgG1 fusion protein CH4Hgamma1.
XX
KW   CD4; IgG1; human; CD4Hgamma1; fusion protein; immunoglobulin; HIV; SIV;
KW   gp120; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .395
FT                   /note= "CD4 extracellular region"
FT   Protein         400. .729
FT                   /note= "IgG1 heavy chain"
XX
PN   US6117656-A.
XX
PD   12-SEP-2000.
XX
PF   07-JUN-1995;   95US-00479353.
XX
PR   22-JAN-1988;   88US-00147351.
PR   23-JAN-1989;   89US-00299596.
PR   09-JUN-1992;   92US-00896781.
PR   12-APR-1993;   93US-00057952.
PR   04-FEB-1994;   94US-00191708.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-586558/55.
DR   N-PSDB; AAA50660.
XX
PT   CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
PT   SIV.
XX
PS   Example 1; Col 13-30; 39pp; English.
XX
CC   The present sequence is that of fusion protein CD4Hgamma1 comprising the
CC   extracellular portion of CD4, which binds to HIV gp120, linked at its C-
CC   terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
CC   encoding CD4 was linked to IgG1 DNA at the Hind3 site upstream of the CH1
CC   region (see AAA50660). Fusion protein CD4Hgamma1 and a nucleic acid
CC   encoding it are claimed. Also claimed are a vector comprising the nucleic
CC   acid, and a method of producing the fusion protein in secreted form using
CC   a transformed host cell. The fusion protein may further comprise a
CC   therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
CC   can be administered to an animal (including humans) for treatment of HIV
CC   or SIV infection, and can also be used in assays for HIV or SIV, imaging
CC   and tissue stains. IgG1 fusion proteins such as CD4Hgamma1 provide both
CC   complement-mediated and cell-mediated immunity
XX
SQ   Sequence 729 AA;
```

```
  Query Match             77.0%;  Score 2079.5;  DB 3;  Length 729;
  Best Local Similarity   58.8%;  Pred. No. 2.5e-107;
  Matches  428;  Conservative    0;  Mismatches    3;  Indels  297;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 ---------------------------------------------------------- 200

Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        201 ---------------------------------------------------------- 200

Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        201 --------PC---------------------------------------------------- 202
                      |
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG 420

Qy        203 ------------PAP---------------------------------------------- 205
                         | |
Db        421 TAALGCLVVSYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY 480

Qy        206 -----------------EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE 243
                               ||||||||||      ||||||||||||||||||||||||||||
Db        481 ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 540

Qy        244 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 600

Qy        304 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 660

Qy        364 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 720

Qy        424 KSLSLSPG 431
              ||||||||
Db        721 KSLSLSPG 728
```

```
RESULT 24
AAY59168
ID   AAY59168 standard; protein; 729 AA.
XX
AC   AAY59168;
XX
```

```
DT   14-MAR-2000  (first entry)
XX
DE   CD4-Ig fusion protein CD4Hgamma1.
XX
KW   HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
KW   secreted protein; SIV infection; medicament.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   CA1340741-C.
XX
PD   14-SEP-1999.
XX
PF   20-JAN-1989;   89CA-00588749.
XX
PR   20-JAN-1989;   89CA-00588749.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-063015/06.
DR   N-PSDB; AAZ48201.
XX
PT   New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
PT   the treatment of HIV or simian immunodeficiency virus infections.
XX
PS   Example 1; Page 25-36; 89pp; English.
XX
CC   The invention provides a fusion gene encoding a fusion protein that
CC   comprises an extracellular CD4 DNA sequence or its fragment which binds
CC   to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
CC   sequence of an Ig heavy or light chain, where the DNA sequence encoding
CC   the variable region has been replaced with the DNA sequence which encodes
CC   extracellular CD4 or its gp120 binding fragment. The fusion protein is
CC   capable of being secreted. The fusion proteins are useful for treating
CC   HIV or SIV infections in animals, preferably humans. They are also useful
CC   for producing medicaments which can be used for treating HIV or SIV
CC   infections in humans. The present sequence represents the fusion protein
CC   CD4Hgamma1 where the CD4 is linked to human IgG1 at the Hind3 site
CC   upstream of the CH1 region
XX
SQ   Sequence 729 AA;

  Query Match            77.0%;  Score 2079.5;  DB 3;  Length 729;
  Best Local Similarity  58.8%;  Pred. No. 2.5e-107;
  Matches  428;  Conservative    0;  Mismatches    3;  Indels  297;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 ------------------------------------------------------------ 200

Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        201 ------------------------------------------------------------ 200

Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        201 --------PC-------------------------------------------------- 202
                     |
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG 420

Qy        203 ------------PAP---------------------------------------------- 205
                         | |
Db        421 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY 480

Qy        206 ----------------EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE 243
                             ||||||||||     |||||||||||||||||||||||||||
Db        481 ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 540

Qy        244 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 600

Qy        304 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 660

Qy        364 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 720

Qy        424 KSLSLSPG 431
              ||||||||
Db        721 KSLSLSPG 728


RESULT 25
AAR46679
ID   AAR46679 standard; protein; 530 AA.
XX
AC   AAR46679;
XX
DT   25-MAR-2003  (revised)
DT   08-AUG-1994  (first entry)
XX
DE   CD4-IgG2 chimeric heavy chain.
XX
KW   CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV;
KW   human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
KW   imaging; detection; targetting; immunoglobulin; IgG.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .204
FT                   /label= CD4 Region.
FT   Region          205. .302
FT                   /label= CH1 Region.
FT   Region          303. .314
FT                   /label= Hinge Region.
FT   Region          315. .423
FT                   /label= CH2 Region.
FT   Region          424. .530
FT                   /label= CH3 Region.
XX
PN   WO9403191-A1.
XX
PD   17-FEB-1994.
XX
PF   06-AUG-1993;   93WO-US007422.
XX
PR   07-AUG-1992;   92US-00927931.
XX
PA   (PROG-) PROGENICS PHARM INC.
XX
PI   Allaway GP,  Maddon PJ;
XX
DR   WPI; 1994-065392/08.
DR   N-PSDB; AAQ55751.
XX
```

```
PT   Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
PT   immuno:conjugates - used to kill HIV-infected cells and to image and
PT   stage HIV infection.
XX
PS   Disclosure; Fig 4; 142pp; English.
XX
CC   A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy
CC   chains and two kappa light chains or CD4-kappa light chains (AAR46680)
CC   linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide
CC   of low to moderate cytotoxicity. The resulting immunoconjugate comprising
CC   the toxin can be used to kill HIV infected cells and to treat HIV
CC   infected subjects to reduce the population of HIV infected cells. It can
CC   also be used to reduce the likelihood of infection. The immunoconjugate
CC   comprising the radionuclide can be used to image HIV infected tissue, to
CC   calculate the stage of HIV infection or the efficacy of an anti-HIV
CC   treatment using the imaging technique and for determining the prognosis
CC   of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 530 AA;

  Query Match             76.8%;  Score 2075;  DB 2;  Length 530;
  Best Local Similarity   76.7%;  Pred. No. 3.2e-107;
  Matches  406;  Conservative   12;  Mismatches   13;  Indels   98;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNRGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV----------------PCPA----------------PEP 207
              |||||||||||||||||||                ||                  |||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 240

Qy        208 ------------------------------------------------------------ 207

Db        241 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK 300

Qy        208 ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                  | | :   ||   : ||||||||||||||||||||||||||||||||||||:|||
Db        301 TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW 360

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              |||||||||||||||||:|||:||||||||:||||||| |||||||||
Db        361 YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKQYKCKVSNKGLPAPIEKTIS 420

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | ||||||||||||||:|:|||||:||||||||||||||||||||||||||||||||||:
Db        421 KTKGQPREPQVYTLPPSREEMTKNQLSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 480

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 529


RESULT 26
AAY51078
ID   AAY51078 standard; protein; 729 AA.
XX
AC   AAY51078;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Human fusion protein CD4H-1.
XX
KW   Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
KW   anti-human immunodeficiency virus; CD4H-1.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6004781-A.
XX
PD   21-DEC-1999.
XX
PF   04-FEB-1994;   94US-00191708.
XX
PR   22-JAN-1988;   88US-00147351.
PR   23-JAN-1989;   89US-00299596.
PR   09-JUN-1992;   92US-00896781.
PR   12-APR-1993;   93US-00057952.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-085792/07.
DR   N-PSDB; AAZ44061.
XX
PT   Fusion protein useful for the treatment of human immunodeficiency virus.
XX
PS   Example 1; Col 15-30; 39pp; English.
XX
CC   This invention describes a novel nucleic acid (I) encoding a fusion
CC   protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
CC   and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC   chain (III). The products pf the invention have anti-human
CC   immunodeficiency virus (HIV) activity and are capable of binding to
CC   gp120. The fusion protein is useful for treating human immunodeficiency
CC   virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC   represents the fusion protein CD4H-1 which is constructed from CD4 linked
CC   to human IgG1 upstream of the CH1 region
XX
SQ   Sequence 729 AA;

  Query Match             76.6%;  Score 2069.5;  DB 3;  Length 729;
  Best Local Similarity   58.7%;  Pred. No. 9.1e-107;
  Matches  427;  Conservative    0;  Mismatches    4;  Indels  297;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              |||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 ------------------------------------------------------------ 200

Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        201 ------------------------------------------------------------ 200

Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        201 --------PC---------------------------------------------------- 202
                      |
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG 420

Qy        203 ------------PAP---------------------------------------------- 205
                         | |
Db        421 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY 480
```

```
Qy        206 ----------------EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE 243
                              ||||||||||     ||||||||| ||||||||||||||||||
Db        481 ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPE 540

Qy        244 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 600

Qy        304 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 660

Qy        364 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 720

Qy        424 KSLSLSPG 431
              ||||||||
Db        721 KSLSLSPG 728
```

RESULT 27
AAP93012
ID AAP93012 standard; protein; 614 AA.
XX
AC AAP93012;
XX
DT 25-MAR-2003 (revised)
DT 03-AUG-1992 (first entry)
XX
DE Genetic construct which encodes CD4 linked to human IgG1 at the Ban1 site
DE downstream from the hinge region (fusion protein CD4Blambda1).
XX
KW Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
KW diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
OS Homo sapiens.
XX
PN EP325262-A.
XX
PD 26-JUL-1989.
XX
PF 20-JAN-1989; 89EP-00100913.
XX
PR 22-JAN-1988; 88US-00147351.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 1989-214472/30.
DR N-PSDB; AAN90360.
XX
PT Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
PT infections or detecting HIV or SIV in sample.
XX
PS Example; Table 5, Page 48-55; 68pp; English.
XX
CC The fusion protein genes of the invention pref. comprises cDNA sequences
CC which encode CD4 or a fragment which binds gp120 ligated to an expression
CC plasmid which encodes an antibody in which the variable region of the
CC gene has been deleted (see Wo87-02671). The CD4 portion of the fusion
CC protein may comprise the complete CD4 sequence, the 370 AA extracellular
CC region and the membrane spanning domain, or the extracellular region. The
CC Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
CC specifically claimed: fusion proteins CD4Hlambda1, CD4Mmu, CD4Pmu,
CC CD4Elambda1, and CD4Mmu (No. 67608), pCD4Plambda (No. 67609) and
CC pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 614 AA;

Query Match 76.1%; Score 2056; DB 1; Length 614;
Best Local Similarity 67.6%; Pred. No. 4.3e-106;
Matches 416; Conservative 1; Mismatches 12; Indels 186; Gaps 4;

```
Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV---------------------------------------- 200
              |||||||||| |||||||||
Db        181 TWTCTVLQNQNKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240

Qy        201 -------------------------------------------PCPAPE---------- 206
                                                          |   |:
Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        207 -----------------PKSCDKTHTC-------------------------------- 216
                              |  ||
Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        217 ---------------------------------------PELLGGPSVFLFPPKPKDTL 236
                                                      ||||||||||||||||||||
Db        361 LNPEAGMWQCLLSDSAQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL 420

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 480

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 DWLNGKEYKCKVSNKALPAPIEKTIS--KGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 538

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 598

Qy        417 LHNHYTQKSLSLSPG 431
              |||||||||||||||
Db        599 LHNHYTQKSLSLSPG 613
```

RESULT 28
AAB19511
ID AAB19511 standard; protein; 616 AA.
XX
AC AAB19511;
XX
DT 09-JAN-2001 (first entry)
XX
DE CD4-IgG1 fusion protein CH4Bgamma1.
XX
KW CD4; IgG1; human; CD4Bgamma1; fusion protein; immunoglobulin; HIV; SIV;
KW gp120; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1. .395
FT /note= "CD4 extracellular region"
FT Protein 400. .616
FT /note= "IgG1 heavy chain"
XX
PN US6117656-A.
XX
PD 12-SEP-2000.
XX

```
PF   07-JUN-1995;   95US-00479353.
XX
PR   22-JAN-1988;   88US-00147351.
PR   23-JAN-1989;   89US-00299596.
PR   09-JUN-1992;   92US-00896781.
PR   12-APR-1993;   93US-00057952.
PR   04-FEB-1994;   94US-00191708.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B;
XX
DR   WPI; 2000-586558/55.
DR   N-PSDB; AAA50664.
XX
PT   CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
PT   SIV.
XX
PS   Example 1; Col 59-70; 39pp; English.
XX
CC   The present sequence is that of fusion protein CD4Bgamma1 comprising the
CC   extracellular portion of CD4, which binds to HIV gp120, linked at its C-
CC   terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
CC   encoding CD4 was linked to IgG1 DNA at the Ban1 site downstream of the
CC   hinge region (see AAA50664). Fusion protein CD4Bgamma1 and a nucleic acid
CC   encoding it are claimed. Also claimed are a vector comprising the nucleic
CC   acid, and a method of producing the fusion protein in secreted form using
CC   a transformed host cell. The fusion protein may further comprise a
CC   therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
CC   can be administered to an animal (including humans) for treatment of HIV
CC   or SIV infection, and can also be used in assays for HIV or SIV, imaging
CC   and tissue stains. IgG1 fusion proteins such as CD4Bgamma1 provide both
CC   complement-mediated and cell-mediated immunity
XX
SQ   Sequence 616 AA;

  Query Match            74.0%;  Score 1999;  DB 3;  Length 616;
  Best Local Similarity  66.8%;  Pred. No. 6.2e-103;
  Matches  410;  Conservative    1;  Mismatches   19;  Indels  184;  Gaps    4;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||| |||||||||||||||||||| |||||||||| ||||  ||||||||||||
Db        121 LVFCLTANSDTHLLQGQSLTLTLESPPCSSPSVQCRSPRCKNIQCCKTLSVSQLELQDSC 180

Qy        181 TWTCTVLQNQKKVEFKIDIV-------------------------------PCP----- 203
              ||||||||||||||||||                               |
Db        181 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTCSGELWW 240

Qy        204 -------------------------APEPK---------------------------- 208
                                      :||
Db        241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300

Qy        209 --------------------SCDKTHTC------------------------------- 216
                                  |  ||
Db        301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360

Qy        217 ----------------------------------------PELLGGPSVFLFPPKPKDTL 236
                                                     ||||||||||||||||||||
Db        361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL 420

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        421 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRYVSVLTVLHQ 480

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DWLNCKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKC 540

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 600

Qy        417 LHNHYTQKSLSLSP 430
              ||||||||||||||
Db        601 LHNHYTQKSLSLSP 614


RESULT 29
AAW35860
ID   AAW35860 standard; protein; 410 AA.
XX
AC   AAW35860;
XX
DT   27-APR-1998  (first entry)
XX
DE   Human CD4:IgG2a constant region fusion protein.
XX
KW   Human; CD4:IgG2a; T lymphocyte veto molecule; chimeric molecule;
KW   targetting polypeptide; suppression; immune response; treatment;
KW   autoimmune disease; allergy; immunological disorder; fusion protein;
KW   immunoglobuin G2a; transplant rejection; constant region.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9737687-A1.
XX
PD   16-OCT-1997.
XX
PF   10-APR-1997;   97WO-US005943.
XX
PR   10-APR-1996;   96US-00630172.
XX
PA   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI   Staerz UD;
XX
DR   WPI; 1997-512419/47.
XX
PT   T lymphocyte veto molecule comprising response cell activating protein -
PT   linked to molecule that targets stimulator cell marker, used for
PT   selective suppression of immune response, e.g. prevention of graft
PT   rejection or treatment of auto-immune disease.
XX
PS   Claim 40; Page 75-76; 309pp; English.
XX
CC   A novel T lymphocyte veto molecule is a chimeric molecule comprising a
CC   protein, e.g. the present sequence, linked to a targetting polypeptide
CC   that binds a molecule, which differentiates a host cell from a tissue
CC   graft cell, or selectively targets a stimulator cell involved in the
CC   autoimmune response. A veto molecule, in which the protein binds a
CC   molecule that targets stimulator cells, can be used to suppress an immune
CC   response and therefore treat autoimmune diseases, e.g. systemic lupus
CC   erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
CC   diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
CC   thyroiditis, Addison's or Grave's diseases and rheumatoid carditis,
CC   allergies and other immunological disorders. Where the protein binds a
CC   molecule that differentiates graft and host cells, the veto molecule can
CC   be used to reduce transplant rejection. The veto molecule provides
CC   specific regulation of particular stimulator cells that can kill graft
CC   cells or respond to autoantigens, but leave other stimulator cells
CC   unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
CC   affecting the other. The veto molecule can be administered locally to
CC   minimise generalised immunosuppression
XX
SQ   Sequence 410 AA;

  Query Match            61.0%;  Score 1647.5;  DB 2;  Length 410;
```

```
  Best Local Similarity   75.8%;  Pred. No. 1.3e-83;
  Matches  316;  Conservative   31;  Mismatches   51;  Indels   19;  Gaps    4;

Qy         26 NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS 60

Qy         86 LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES 120

Qy        146 PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV----- 200
              ||||||||||||||||||||||||||||||:||| ||||||||||||||||||
Db        121 PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDAGTWICTVLQNQKKVEFKIDIVVLAEP 180

Qy        201 ------PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 254
                   |||   |  |       | ||||||||:|||| || |||| :| |||||||||  :
Db        181 RGPTIKPCP---PCKC----PAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSED 233

Qy        255 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314
              ||:|: :|:|: |||| |:|:   | |||  |||| | : ||||::|||:||||:|| ||
Db        234 DPDVQISWFVNNVEVHTAQTQTHREDYNSRLRVVSALPIQHQDWMSGKEFKCKVNNKDLP 293

Qy        315 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
              ||||:|||| ||  | |||| |||  :|:|| ||:|||:|  | | || ||| :||: |
Db        294 APIERTISKPKGSVRAPQVYVLPPP-EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTEL 352

Qy        375 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||| | ||||||||:|:|||| |:|  | : | :||||:|| ||||:| || | :||
Db        353 NYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 409


RESULT 30
AAR20634
ID   AAR20634 standard; protein; 343 AA.
XX
AC   AAR20634;
XX
DT   22-MAY-1992  (first entry)
XX
DE   Chimeric protein V1V2-hCH2-KA.
XX
KW   CD4; LTI; Streptomyces longisporous; HIV gp120; AIDS; IgGl; T cell;
KW   immunoglobulin; surface glycoprotein; virus; MHC class II.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   28. .29
FT                   /label= signal_cleavage
FT   Protein         29. .213
FT                   /label= V1V2
FT   Region          214. .228
FT                   /label= hinge
FT   Protein         229. .343
FT                   /label= CH2
XX
PN   WO9200985-A.
XX
PD   23-JAN-1992.
XX
PF   11-JUL-1990;   90US-00551584.
XX
PR   11-JUL-1990;   90US-00551584.
PR   05-MAR-1991;   91US-00665218.
XX
PA   (SMIK ) SMITHKLINE BEECHAM.
XX
PI   Brawner ME,  Fornwald JA,  Arthos J;
XX
DR   WPI; 1992-056814/07.
DR   N-PSDB; AAQ20907.
XX
PT   Nucleic acid sequences for production of CD4 chimeric protein - used to
PT   transfect streptomyces, contg. LTI signal sequence linked to pro-peptide
PT   sequence facilitating peptide cleavage.
XX
PS   Claim 16; Page 23; 47pp; English.
XX
CC   The sequence was deduced by sequencing the plasmid vector V1V2-hCH2- KA
CC   in S. lividans strain 1326. The protein has domains contg. peptides of
CC   different function. It contains a CD4 chimera (V1V2) in which the carboxy
CC   terminal portion of the protein consists of a murine immunoglobulin light
CC   chain constant region, linked to the signal peptide of Streptomyces LTI,
CC   modified at its N-terminus to include Lys-Arg. Also included is the IgGl
CC   constant region comprising the hinge and CH2 motifs. Human IgGl is the
CC   most effective immunoglobulin subclass at mediating cell killing by both
CC   complement and ADCC. The CD4 chimeric proteins may be expressed in
CC   bacterial hosts. The fusion of the human Ig constant region lacking the
CC   CH3 domain, and the LTI CD4 protein increases the stability of the CD4,
CC   thus increasing the serum half life and/or potency against HIV infection
CC   and inhibit virus-induced cell fusion, relative to soluble CD4. By
CC   altering only one amino acid at position 2 near the N terminal of CD4 (V1
CC   region) from Lys to Ala, a heterologous protein is expressed which is
CC   efficiently secreted and correctly processed to remove the entire LTI
CC   signal sequence, but which still retains the gp120 binding capacity. By
CC   modifying the pro-peptide you avoid deleterious effects of additional
CC   amino acids on the function of the protein. See also AAR20635,6
XX
SQ   Sequence 343 AA;

  Query Match             57.2%;  Score 1546;  DB 2;  Length 343;
  Best Local Similarity   93.2%;  Pred. No. 4.5e-78;
  Matches  300;  Conservative    0;  Mismatches   12;  Indels   10;  Gaps    2;

Qy         19 LPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND 78
              |  |     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 LTGAALAKAVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND 81

Qy         79 RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 141

Qy        139 LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID 201

Qy        199 IV-----PCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
              ||          ||||||||||      ||||||||||||||||||||||||||||||
Db        202 IVVLAFQKASKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 261

Qy        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 321

Qy        309 SNKALPAPIEKTISKAKGQPRE 330
              ||||||||||||||||||||||
Db        322 SNKALPAPIEKTISKAKGQPRE 343


RESULT 31
AAR89441
ID   AAR89441 standard; peptide; 254 AA.
XX
AC   AAR89441;
XX
DT   26-SEP-1996  (first entry)
XX
DE   IgG1 hinge, CH2 and CH3 domains.
XX
KW   CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
KW   human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
KW   dendritic cell; therapy; mammal; infection.
XX
OS   Homo sapiens.
XX
```

```
PN   WO9603883-A1.
XX
PD   15-FEB-1996.
XX
PF   26-JUL-1995;   95WO-US009468.
XX
PR   02-AUG-1994;   94US-00284391.
PR   24-FEB-1995;   95US-00394388.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Banapour B,  Romeo C,  Kolanus W;
XX
DR   WPI; 1996-129034/13.
DR   N-PSDB; AAT10780.
XX
PT   Membrane-bound chimeric receptor comprising extracellular portion
PT   including CD4 fragment - cells expressing receptor can be used for
PT   treatment of HIV infection.
XX
PS   Claim 3; Fig 25; 134pp; English.
XX
CC   This sequence represents the human IgG1 hinge, CH2 and CH3 domains. This
CC   sequence is included in the membrane bound proteinaceous chimeric
CC   receptor of the invention. Alternatively the transmembrane region of the
CC   chimeric receptor contains a portion of the CD7, CD5 or CD34
CC   transmembrane domains. The extracellular portion of the chimeric receptor
CC   contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4
CC   sequence) which specifically recognises and binds HIV-infected cells, but
CC   does not mediate HIV infection. The extracellular domain of the receptor
CC   is separated from the cell membrane by 48 or 72 angstroms, or by one or
CC   more proteinaceous alpha-helices. The cells expressing the receptor are
CC   preferably T cells, B cells, neutrophils, or dendritic cells. The
CC   therapeutic cells expressing the chimeric receptor are administered to a
CC   mammal to treat HIV infection
XX
SQ   Sequence 254 AA;

  Query Match             49.5%;  Score 1338.5;  DB 2;  Length 254;
  Best Local Similarity   98.0%;  Pred. No. 1.1e-66;
  Matches  249;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    1;

Qy        206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
              ||||||||||     ||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy        261 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        321 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        381 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 240

Qy        441 AQDGELDGLWTTDP 454
              ||||||||||||||
Db        241 AQDGELDGLWTTDP 254


RESULT 32
AAR78667
ID   AAR78667 standard; protein; 254 AA.
XX
AC   AAR78667;
XX
DT   11-APR-1996  (first entry)
XX
DE   IgG1 hinge, CH2 and CH3 domains.
XX
KW   Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis;
KW   human immunodeficiency virus; adoptive immunotherapy; IgG1.
XX
OS   Homo sapiens.
XX
PN   WO9521528-A1.
XX
PD   17-AUG-1995.
XX
PF   12-JAN-1995;   95WO-US000454.
XX
PR   14-FEB-1994;   94US-00195395.
PR   02-AUG-1994;   94US-00284391.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Banapour B,  Romeo C,  Kolanus W;
XX
DR   WPI; 1995-292893/38.
DR   N-PSDB; AAQ96101.
XX
PT   Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
PT   cells.
XX
PS   Claim 3; Fig 25; 118pp; English.
XX
CC   Human IgG1 hinge, CH2 and CH3 domains (AAR78668) are used in the
CC   construction of a chimeric receptor utilised in the targeted cytolysis of
CC   HIV-infected cells. The chimeric receptor comprises the extracellular
CC   domain (pref. amino acids 1-394 or 1-200) of CD4 linked via the CD7
CC   transmembrane domain to an intracellular portion, e.g. of T-cell receptor
CC   protein zeta. The IgG1 portion of the chimeric receptor is encoded by the
CC   DNA sequence given in AAQ96101
XX
SQ   Sequence 254 AA;

  Query Match             49.3%;  Score 1332.5;  DB 2;  Length 254;
  Best Local Similarity   97.6%;  Pred. No. 2.3e-66;
  Matches  248;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    1;

Qy        206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
              ||||||||||     ||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy        261 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 320
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSKKALPAPIEKT 120

Qy        321 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        381 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 240

Qy        441 AQDGELDGLWTTDP 454
              ||||||||||||||
Db        241 AQDGELDGLWTTDP 254


RESULT 33
ADD13790
ID   ADD13790 standard; protein; 400 AA.
XX
AC   ADD13790;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Plasmid pBS loxP-IgG1/pBS loxP-IgG1delta350/pBS loxPIgGdeltaCH1 protein.
XX
KW   library; transfection; humanized monoclonal antibody; antigen;
KW   T cell receptor; circular.
```

```
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .97
FT                   /note= "Human IgG1 CH3"
FT   Region          98. .112
FT                   /note= "Human IgG1 hinge"
FT   Region          113. .222
FT                   /note= "human IgG1 CH2"
FT   Region          223. .329
FT                   /note= "Human IgG1 CH3"
FT   Region          330. .373
FT                   /note= "Murine IgG1 M1"
FT   Region          374. .400
FT                   /note= "Murine IgG2 M2"
XX
PN   EP1298207-A1.
XX
PD   02-APR-2003.
XX
PF   01-OCT-2001; 2001EP-00123596.
XX
PR   01-OCT-2001; 2001EP-00123596.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Breitling F,  Moldenhauer G,  Poustka A,  Kuehlwein T;
XX
DR   WPI; 2003-383833/37.
XX
PT   Preparing library of protein-producing eukaryotic cells, useful for
PT   producing humanized high-affinity antibodies, comprises introducing
PT   specific recombination signals into chromosomal gene loci and integrating
PT   a variety of DNA sequences.
XX
PS   Example 19; Fig 16; 75pp; German.
XX
CC   This invention describes a novel method of preparing a library of protein
CC   -producing eukaryotic cells comprising (a) introducing specific
CC   recombination signals into one or two chromosomal gene loci, (b)
CC   Expanding at least one of the modified cells, (c) Transfecting many
CC   different DNA sequences, each flanked by recombination signals, into the
CC   expanded cells and (d) Integrating the DNA sequences into the gene loci
CC   on the basis of the recombination signals and the appropriate
CC   recombinase. The resulting cells express different proteins, each from an
CC   integrated DNA sequence and the proteins are bound to the cell surface.
CC   The method is particularly used to produce libraries of humanized
CC   monoclonal antibodies, for selection of those with affinity for
CC   particular antigens and useful for diagnostic or therapeutic use.
CC   Libraries of T cell receptors may also be prepared. The method produces
CC   libraries of high diversity; provides easy, quick and automatable
CC   selection from a large number of proteins, allows relatively simple
CC   alteration of the expressed gene (e.g. fusion to other protein-coding
CC   sequences), is suitable for large scale protein production and allows
CC   simple verification and characterization of selected cell lines. The
CC   method does not require incorporation of a resistance marker. This
CC   sequence represents the construct pBS loxP-IgG1/pBS loxP-IgG1delta350/pBS
CC   loxPIgGdeltaCH1 described in the disclosure of the invention.
XX
SQ   Sequence 400 AA;

  Query Match             49.1%;  Score 1327.5;  DB 7;  Length 400;
  Best Local Similarity   75.4%;  Pred. No. 7.1e-66;
  Matches  266;  Conservative    8;  Mismatches   22;  Indels   57;  Gaps    7;

Qy        151 PSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG---- 180
              |||   :|  |:  ||              : ::||               || ||
Db          5 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 64

Qy        181 --------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLG 221
                           |: | |  | |    |:|       ||||||||||     |||||
Db         65 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 118

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        119 GPSVFLFPPKPKDTLMISRTPQVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 178

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 238

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 298

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSP--GLQLDETCAEAQDGELDGLWTT 452
              |||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        299 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGLQLDETCAEAQDGELDGLWTT 351


RESULT 34
ADD13781
ID   ADD13781 standard; protein; 401 AA.
XX
AC   ADD13781;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Plasmid pBS MbIgG1M/ pBS MhIgG1Mdelta250 protein.
XX
KW   library; transfection; humanized monoclonal antibody; antigen;
KW   T cell receptor; circular.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .97
FT                   /note= "human IgG1 CH1"
FT   Region          98. .112
FT                   /note= "human IgG1 hinge"
FT   Region          113. .222
FT                   /note= "human IgG1 CH2"
FT   Region          223. .330
FT                   /note= "human IgG1 CH3"
FT   Region          331. .374
FT                   /note= "murine IgG1 M1"
FT   Region          375. .401
FT                   /note= "murine IgG1 M2"
XX
PN   EP1298207-A1.
XX
PD   02-APR-2003.
XX
PF   01-OCT-2001; 2001EP-00123596.
XX
PR   01-OCT-2001; 2001EP-00123596.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Breitling F,  Moldenhauer G,  Poustka A,  Kuehlwein T;
XX
DR   WPI; 2003-383833/37.
DR   N-PSDB; ADD13780.
XX
PT   Preparing library of protein-producing eukaryotic cells, useful for
PT   producing humanized high-affinity antibodies, comprises introducing
PT   specific recombination signals into chromosomal gene loci and integrating
PT   a variety of DNA sequences.
XX
PS   Example 1; Fig 12B; 75pp; German.
XX
```

```
CC   This invention describes a novel method of preparing a library of protein
CC   -producing eukaryotic cells comprising (a) introducing specific
CC   recombination signals into one or two chromosomal gene loci, (b)
CC   Expanding at least one of the modified cells, (c) Transfecting many
CC   different DNA sequences, each flanked by recombination signals, into the
CC   expanded cells and (d) Integrating the DNA sequences into the gene loci
CC   on the basis of the recombination signals and the appropriate
CC   recombinase. The resulting cells express different proteins, each from an
CC   integrated DNA sequence and the proteins are bound to the cell surface.
CC   The method is particularly used to produce libraries of humanized
CC   monoclonal antibodies, for selection of those with affinity for
CC   particular antigens and useful for diagnostic or therapeutic use.
CC   Libraries of T cell receptors may also be prepared. The method produces
CC   libraries of high diversity; provides easy, quick and automatable
CC   selection from a large number of proteins, allows relatively simple
CC   alteration of the expressed gene (e.g. fusion to other protein-coding
CC   sequences), is suitable for large scale protein production and allows
CC   simple verification and characterization of selected cell lines. The
CC   method does not require incorporation of a resistance marker. This
CC   sequence represents the construct MbIgG1M/ pBS MhIgG1Mdelta250 described
CC   in the disclosure of the invention.
XX
SQ   Sequence 401 AA;

  Query Match             48.7%;  Score 1315;  DB 7;  Length 401;
  Best Local Similarity   75.1%;  Pred. No. 3.5e-65;
  Matches  266;  Conservative    7;  Mismatches   23;  Indels   58;  Gaps    8;

Qy        151 PSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG---- 180
              |||   :|  |:  ||             : ::||               || ||
Db          5 PSVFPLAPSSKSTSGGTAALGCLVXDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 64

Qy        181 --------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLG 221
                          |: | |  | |    |:|       ||||||||||     |||||
Db         65 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 118

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 178

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        179 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPXEKTISKAKGQPREPQVYTLPPSRD 238

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 298

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSL-SLSP--GLQLDETCAEAQDGELDGLWTT 452
              |||||||||||||||||||||||| ||||  ||||||||||||||||||||||
Db        299 WQQGNVFSCSVMHEALHNHYTQKSLSSLSPGKGLQLDETCAEAQDGELDGLWTT 352


RESULT 35
ABJ37104
ID   ABJ37104 standard; protein; 437 AA.
XX
AC   ABJ37104;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Concatameric immunoadhesion human protein sequence SEQ ID No 14.
XX
KW   Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW   antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW   dimeric protein; inflammation; septicaemia; cytotoxicity;
KW   rheumatoid arthritis; cachexia; inflammation; human.
XX
OS   Homo sapiens.
XX
PN   WO2003010202-A1.
XX
PD   06-FEB-2003.
XX
PF   26-JUL-2002; 2002WO-KR001427.
XX
PR   26-JUL-2001; 2001KR-00045028.
XX
PA   (MEDE-) MEDEXGEN CO LTD.
XX
PI   Chung Y,  Han J,  Lee H,  Choi E,  Kim J;
XX
DR   WPI; 2003-229639/22.
DR   N-PSDB; ABT32047.
XX
PT   New concatameric protein having two soluble domains, useful for
PT   diagnosing and treating disorders associated with the dimeric protein or
PT   its glycosylated form, such as inflammation, septicemia, rheumatoid
PT   arthritis and cachexia.
XX
PS   Disclosure; Page 156-158; 211pp; English.
XX
CC   The invention relates to a novel concatameric protein comprising two
CC   soluble domains, in which an N-terminus of a soluble domain of a
CC   biologically active protein is linked to a C-terminus of an identical
CC   soluble domain or a different soluble domain of a biologically active
CC   protein. The methods and compositions of the present invention are useful
CC   for the diagnosis and treatment of disorders associated with dimeric
CC   protein or its glycosylated form, such as inflammation, septicaemia,
CC   cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC   related diseases. This sequence represents the human concatameric protein
CC   of the invention
XX
SQ   Sequence 437 AA;

  Query Match             47.6%;  Score 1287.5;  DB 6;  Length 437;
  Best Local Similarity   64.7%;  Pred. No. 1.3e-63;
  Matches  273;  Conservative   22;  Mismatches   62;  Indels   65;  Gaps   11;

Qy         35 DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL 94
              | ::   |: :||  ||  :            :|  |   ||              |  |
Db         55 DDIKWEKTSDKKKIAQFRKEKE----------TFKEKDTYKLFK------------NGTL 92

Qy         95 IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ-----------SLTLT 142
              ||:|| :| | |   : | : |   :| |         :| :             : |||
Db         93 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-------IQERVSKPKISWTCINTTLT 145

Qy        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT--------CTVLQNQKKVE 194
              |   |: | :          | || | :||  :  :  ||         ||   |:   |
Db        146 CEVMNGTDPELNL-------YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 195

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
                ::  | ||| ||||||||||     ||||||||||||||||||||||||||||||||
Db        196 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 254

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 314

Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 374

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 434

Qy        430 PG 431
              ||
Db        435 PG 436


RESULT 36
AAR42162
ID   AAR42162 standard; protein; 461 AA.
XX
```

```
AC   AAR42162;
XX
DT   25-MAR-2003  (revised)
DT   27-APR-1994  (first entry)
XX
DE   Anti-HIV-1 recombinant antibody 447-52D heavy chain.
XX
KW   Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW   HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW   acquired immune deficiency syndrome; chimeric antibody;
KW   surface glycoprotein gp120; V3 loop.
XX
OS   Homo sapiens.
XX
PN   WO9319785-A1.
XX
PD   14-OCT-1993.
XX
PF   23-MAR-1993;   93WO-US002629.
XX
PR   01-APR-1992;   92US-00861701.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Emini EA,  Conley AJ,  Mark GE,  Johnson LS,  Pfarr DS;
XX
DR   WPI; 1993-336600/42.
DR   N-PSDB; AAQ49834.
XX
PT   New recombinant human antibody - with HIV neutralising activity against
PT   at least two isolates, useful for preventing or treating infection in
PT   diagnosis, etc.
XX
PS   Example 9; Fig 2A; 154pp; English.
XX
CC   EBV-transformed cell lines and mouse-human heterohybridomas producing
CC   human MAbs specific for the gp120 V3 loop of HIV-1 MN isolate were
CC   obtained. MAb 447-52D was found to recognise the tetrapeptide motif GPGR,
CC   i.e. the Principal Neutralising Determinant common to the V3 loop of
CC   different HIV isolates. A recombinant Ab was produced in which the H
CC   chain V region was derived from 447-52D and to which a signal sequence
CC   and a H chain intronic sequence are appended, fused to a fragment contg.
CC   a short intronic segment of the human gamma 1 C region and the human
CC   gamma 1 encoding domain in its genomic form. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 461 AA;

  Query Match             47.6%;  Score 1287;  DB 2;  Length 461;
  Best Local Similarity   59.1%;  Pred. No. 1.5e-63;
  Matches  276;  Conservative   30;  Mismatches   79;  Indels   82;  Gaps   11;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND--------- 78
              | | | :: ||| ||      :  :|     | |   |  ::      |
Db         11 LVKPGGSLRLTCVASGFTFSDVWLNWVRQAPGKGLEWVGRIKSRTDGGTTDYAASVKGRF 70

Qy         79 ---RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ 135
                 | ||: :|: | |      :|| ||:  | |  :       ::: |:: :   : :
Db         71 TISRDDSKNTLYLQMN------SLKTEDTAVYSCTTDG-----FIMIRGVSEDYYYYYMD 119

Qy        136 --GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------- 172
               |:  |:|: |     |||   :|  |:  ||             : ::||
Db        120 VWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 179

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                    || ||                 |: | |  | |    |:|       ||||
Db        180 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKS 233

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 293

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 353

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 413

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        414 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 460


RESULT 37
AAO18400
ID   AAO18400 standard; protein; 449 AA.
XX
AC   AAO18400;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Mature humanised murine CBE11 heavy chain variable domain.
XX
KW   Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;
KW   neoplasia; LT-beta-R; light chain; heavy chain; variable region.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO200230986-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US032140.
XX
PR   13-OCT-2000; 2000US-0240285P.
PR   13-MAR-2001; 2001US-0275289P.
PR   21-JUN-2001; 2001US-0299987P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Garber E,  Lyne P,  Saldanha JW;
XX
DR   WPI; 2002-583337/62.
XX
PT   New humanized anti-lymphotoxin-beta receptor antibody, useful for
PT   treating or reducing the advancement, severity or effects of neoplasia,
PT   particularly solid tumors (i.e. carcinomas) including colorectal cancer
PT   and breast cancer.
XX
PS   Example 5; Page 25-26; 41pp; English.
XX
CC   The present invention relates to humanised anti-lymphotoxin beta receptor
CC   (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
CC   binding antibody CBE11 and can be used to treat neoplasia in humans. The
CC   present sequence is a humanised murine CBE11 heavy chain variable region
XX
SQ   Sequence 449 AA;

  Query Match             47.6%;  Score 1285.5;  DB 5;  Length 449;
  Best Local Similarity   59.0%;  Pred. No. 1.7e-63;
  Matches  275;  Conservative   29;  Mismatches   71;  Indels   91;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFLTKGPSKLN---- 77
              | | | :: |:| ||          :|      |    :  : : ||: |  |  :
Db         11 LVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSY-TYYPDSVKGRFT 69

Qy         78 -DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ- 135
               | ::: ||:      | : :|: ||:  | |  |:              | : :
Db         70 ISRDNAKNSLY------LQMSSLRAEDTAVYYCAREE-------------NGNFYYFDY 109

Qy        136 -GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               ||  |:|: |     |||   :|  |:  ||             : ::||
Db        110 WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 169
```

```
Qy        173 ----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
              || ||                   |: | |  | |    |:|       |||||
Db        170 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 223

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 283

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 343

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 403

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        404 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449
```

RESULT 38
AAR42066
ID AAR42066 standard; protein; 459 AA.
XX
AC AAR42066;
XX
DT 25-MAR-2003 (revised)
DT 29-APR-1994 (first entry)
XX
DE Human anti-HBs heavy chain.
XX
KW Antibody; Ab; light; heavy; chain; hepatitis B; HB; surface antigen.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .9
FT		/label= sig_peptide
FT	Protein	10. .459
FT		/label= mat_protein

XX
PN WO9320205-A1.
XX
PD 14-OCT-1993.
XX
PF 30-MAR-1993; 93WO-JP000396.
XX
PR 30-MAR-1992; 92JP-00074678.
XX
PA (SUNR) SUNTORY LTD.
XX
PI Kurihara T, Matsukura S, Tsuruoka N, Arima K, Nishihara T;
XX
DR WPI; 1993-336913/42.
DR N-PSDB; AAQ49944.
XX
PT Human anti-hepatitis B surface antigen antibody gene - can be used to
PT produce L and H chains of the antibody in large quantity.
XX
PS Disclosure; Fig 6-8; 46pp; Japanese.
XX
CC Polynucleotides encoding the L and H chains of human anti-HBs Ab are
CC given in AAQ49943-Q49944. The Ab can be easily produced in large
CC quantities for therapeutic use. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 459 AA;

Query Match 47.5%; Score 1284.5; DB 2; Length 459;
Best Local Similarity 59.4%; Pred. No. 2e-63;
Matches 280; Conservative 30; Mismatches 68; Indels 93; Gaps 17;

```
Qy         25 GNKVVLGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKIL---GNQGSFL--TK 71
              |  ||  : | :: |:| ||     |  ||      |    : ::   ||  :   |
Db         17 GGGVV--QPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFYADSVK 74

Qy         72 GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   :: | :|: :|:     | :|:|: ||:  | | : ||       :|:
Db         75 GRFTIS-RDNSKNTLY------LEVKSLQTEDTGVYYC-IRDQ-------TYGV------ 113

Qy        132 HLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS---- 172
              |    ||   :|: |     |||   :|  |:  ||            : ::||
Db        114 HRFDSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 173

Qy        173 ---------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAP 205
                       || ||                   |: | |  | |    |:|
Db        174 ALASGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKV 227

Qy        206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
              ||||||||||     ||||||||||||||||||||||||||||||||||||||||||||
Db        228 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 287

Qy        261 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 347

Qy        321 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 407

Qy        381 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 458
```

RESULT 39
AAW05829
ID AAW05829 standard; protein; 446 AA.
XX
AC AAW05829;
XX
DT 16-OCT-2003 (revised)
DT 27-JAN-1997 (first entry)
XX
DE Humanised 1D10 antibody heavy chain.
XX
KW B-cell lymphoma; humanised antibody; bispecific antibody; myeloma;
KW leukaemia; hybridoma; monoclonal antibody.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX

FH	Key	Location/Qualifiers
FT	Domain	1. .116
FT		/label= Variable_domain
FT	Region	31. .35
FT		/label= CDR1
FT	Region	50. .65
FT		/label= CDR2
FT	Region	98. .105
FT		/label= CDR3
FT	Domain	117. .214
FT		/label= CH1
FT	Domain	215. .229
FT		/label= Hinge
FT	Domain	230. .339
FT		/label= CH2
FT	Domain	340. .446
FT		/label= CH3

XX
PN WO9626964-A1.
XX
PD 06-SEP-1996.

```
XX
PF   29-FEB-1996;   96WO-US002754.
XX
PR   01-MAR-1995;   95US-00397411.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
PA   (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX
PI   Weiner G,  Gingrich R,  Link BK,  Tso JY;
XX
DR   WPI; 1996-412742/41.
XX
PT   New bi-specific antibody reactive with both T or NK cells and malignant B
PT   cells - also their humanised forms and hybridomas producing them, useful
PT   for treating or preventing leukaemia, lymphoma and myeloma.
XX
PS   Example 4; Fig 4e; 85pp; English.
XX
CC   The humanised 1D10 antibody heavy chain (AAW05829) includes a variable
CC   region (see also AAW05823) consisting of human R3.5HG heavy chain
CC   variable region framework and complementarity determining regions from
CC   the murine 1D10 antibody specific for a 28/32 kDa antigen found on the
CC   surface of malignant B-cells. It can be coexpressed with humanised 1D10
CC   light chain (see also AAW05828) in mammalian host cells. Bispecific
CC   antibodies can be constructed that include a first binding fragment
CC   comprising humanised M291 heavy and light chain variable regions (see
CC   also AAW05826, AAW05830), and a second binding fragment comprising
CC   humanised 1D10 heavy and light chain variable regions. Such antibodies
CC   are reactive with both T or NK cells and malignant B cells, and have
CC   therapeutic and diagnostic applns. (Updated on 16-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 446 AA;

  Query Match             47.5%;  Score 1282.5;  DB 2;  Length 446;
  Best Local Similarity   59.8%;  Pred. No. 2.5e-63;
  Matches  274;  Conservative   25;  Mismatches   80;  Indels   79;  Gaps   10;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL- 86
Db         11 LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 70

Qy         87 --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
Db         71 KDTSKNQVSLKLNSLTAADTAVYYC----------------ARNDRYAMDYWGQGTLVT 113

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
Db        114 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHFTPAVL 173

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
Db        174 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP 227

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
Db        228 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 287

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
Db        288 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 347

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
Db        348 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 407

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        408 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 445


RESULT 40
ABJ37106
ID   ABJ37106 standard; protein; 617 AA.
XX
AC   ABJ37106;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Concatameric immunoadhesion human protein sequence SEQ ID No 18.
XX
KW   Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW   antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW   dimeric protein; inflammation; septicaemia; cytotoxicity;
KW   rheumatoid arthritis; cachexia; inflammation; human.
XX
OS   Homo sapiens.
XX
PN   WO2003010202-A1.
XX
PD   06-FEB-2003.
XX
PF   26-JUL-2002; 2002WO-KR001427.
XX
PR   26-JUL-2001; 2001KR-00045028.
XX
PA   (MEDE-) MEDEXGEN CO LTD.
XX
PI   Chung Y,  Han J,  Lee H,  Choi E,  Kim J;
XX
DR   WPI; 2003-229639/22.
DR   N-PSDB; ABT32049.
XX
PT   New concatameric protein having two soluble domains, useful for
PT   diagnosing and treating disorders associated with the dimeric protein or
PT   its glycosylated form, such as inflammation, septicemia, rheumatoid
PT   arthritis and cachexia.
XX
PS   Claim 6; Page 171-174; 211pp; English.
XX
CC   The invention relates to a novel concatameric protein comprising two
CC   soluble domains, in which an N-terminus of a soluble domain of a
CC   biologically active protein is linked to a C-terminus of an identical
CC   soluble domain or a different soluble domain of a biologically active
CC   protein. The methods and compositions of the present invention are useful
CC   for the diagnosis and treatment of disorders associated with dimeric
CC   protein or its glycosylated form, such as inflammation, septicaemia,
CC   cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC   related diseases. This sequence represents the human concatameric protein
CC   of the invention
XX
SQ   Sequence 617 AA;

  Query Match             47.5%;  Score 1282.5;  DB 6;  Length 617;
  Best Local Similarity   64.5%;  Pred. No. 3.5e-63;
  Matches  272;  Conservative   22;  Mismatches   63;  Indels   65;  Gaps   11;

Qy         35 DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL 94
Db        235 DDIKWEKTSDKKKIAQFRKEKE----------TFKEKDTYKLFK------------NGTL 272

Qy         95 IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ-----------SLTLT 142
Db        273 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-------IQERVSKPKISWTCINTTLT 325

Qy        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT--------CTVLQNQKKVE 194
Db        326 CEVMNGTDPELNL-------YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 375

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
Db        376 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 434

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
Db        435 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVCHQDWLNGKEYKCKVS 494
```

```
Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 554

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 614

Qy        430 PG 431
              ||
Db        615 PG 616
```

RESULT 41
ABJ37108
ID ABJ37108 standard; protein; 617 AA.
XX
AC ABJ37108;
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion human protein sequence SEQ ID No 22.
XX
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicaemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.
XX
OS Homo sapiens.
XX
PN WO2003010202-A1.
XX
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
PR 26-JUL-2001; 2001KR-00045028.
XX
PA (MEDE-) MEDEXGEN CO LTD.
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
DR WPI; 2003-229639/22.
DR N-PSDB; ABT32051.
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
PS Claim 27; Page 188-191; 211pp; English.
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicaemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents the human concatameric protein
CC of the invention
XX
SQ Sequence 617 AA;

```
  Query Match             47.5%;  Score 1282.5;  DB 6;  Length 617;
  Best Local Similarity   64.5%;  Pred. No. 3.5e-63;
  Matches  272;  Conservative   22;  Mismatches   63;  Indels   65;  Gaps   11;

Qy         35 DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL 94
              | ::   |: :||  ||  :          :|  |   ||             |  |
Db        235 DDIKWEKTSDKKKIAQFRKEKE----------TFKEKDTYKLFK-----------NGTL 272

Qy         95 IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ----------SLTLT 142
               ||:|| :| | |   : | | : |   :| |         :| :          : |||
Db        273 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-------IQERVSKPKISWTCINTTLT 325

Qy        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT--------CTVLQNQKKVE 194
               |   |: | :          |:|| | :||  :  :  ||        ||   |:   |
Db        326 CEVMNGTDPELNL-------YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 375

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
               :: | ||| ||||||||||||     ||||||||||||||||||||||||||||||||
Db        376 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 434

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        435 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVCHQDWLNGKEYKCKVS 494

Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 554

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 614

Qy        430 PG 431
              ||
Db        615 PG 616
```

RESULT 42
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX

```
SQ   Sequence 582 AA;

  Query Match             47.4%;  Score 1282;  DB 4;  Length 582;
  Best Local Similarity   57.5%;  Pred. No. 3.5e-63;
  Matches  279;  Conservative   32;  Mismatches   74;  Indels  100;  Gaps   14;

Qy         32 KKGDTVELTCTAS--QKKSIQFHWKNSNQIKIL--------GNQGSFLT---KGPSKLND 78
              | | :::::| ||           |       | |         |  |:: :   ||   ::
Db         13 KPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYSDSVKGRFTIS- 71

Qy         79 RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
              | ::: :|:      | :::|: |||  | |       |:|  :   :          ||
Db         72 RDNAKNTLY------LQMRSLRSEDSAMYFC------TRVKLGTYYFDS-------WGQG 112

Qy        139 LTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------------- 172
               |||: |     |||   :|  |:  ||             : ::||
Db        113 TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172

Qy        173 QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH 214
                 || ||                 |: | |  | |    |:|       |||||||||
Db        173 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTH 226

Qy        215 TC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269
              ||     ||||||||||||||||||||||||||||||||||||||||||||||||||||| .
Db        227 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 286

Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 346

Qy        330 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 406

Qy        390 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------------LQLDET 437
              |||||||||||||||||||||||||||||||||||||||||||            |||:
Db        407 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHL 466

Qy        438 CAEAQ 442
                : |
Db        467 LLDLQ 471


RESULT 43
AAU07745
ID   AAU07745 standard; protein; 461 AA.
XX
AC   AAU07745;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Humanised monoclonal antibody Hu266, heavy chain.
XX
KW   Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW   Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW   gene therapy.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .461
FT                   /label= Mature_Hu266_heavy_chain
FT                   /note= "This sequence is specifically claimed in claim
FT                   17"
XX
PN   WO200162801-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US006191.
XX
PR   24-FEB-2000; 2000US-0184601P.
PR   08-DEC-2000; 2000US-0254465P.
PR   08-DEC-2000; 2000US-0254498P.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM,  Demattos R,  Bales KR,  Paul SM,  Tsurushita N;
PI   Vasquez M;
XX
DR   WPI; 2001-550087/61.
XX
PT   New humanized antibody for the treatment of Alzheimer's comprises the
PT   inhibition and reduction of the formation of amyloid plaques.
XX
PS   Example 13; Fig 5; 63pp; English.
XX
CC   The invention relates a humanised antibody that specifically binds an
CC   epitope contained within positions 13-28 of amyloid beta peptide, Abeta.
CC   The antibody is useful to inhibit and reduce the formation of amyloid
CC   plaques or the effects of toxic soluble Abeta species in humans their
CC   fragments are used for the manufacture of a medicant. This includes the
CC   prolonged expression of recombinant sequences of them in human tissues
CC   for the treatment of clinical/pre-clinical Alzheimer's disease, Down's
CC   syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the
CC   antibody is used to sequester Abeta into plasma, brain or cerebrospinal
CC   fluid to prevent/reverse accumulation of the Abeta peptide within the
CC   brain thereby improving cognition. The present sequence is the heavy
CC   chain of a humanised monoclonal antibody, Hu266, based on the mouse
CC   antibody 266
XX
SQ   Sequence 461 AA;

  Query Match             47.4%;  Score 1280.5;  DB 4;  Length 461;
  Best Local Similarity   57.2%;  Pred. No. 3.3e-63;
  Matches  282;  Conservative   30;  Mismatches   86;  Indels   95;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS-- 56
              || |:    |:|||:  |       :   | : | :: |:| ||          |
Db          1 MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP 60

Qy         57 -------NQIKILGNQGSF--LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTY 107
                    ||  :||   :    ||   :: | ::: :|: | |       :|: ||:  |
Db         61 GKGLELVAQINSVGNSTYYPDTVKGRFTIS-RDNAKNTLYLQMN------SLRAEDTAVY 113

Qy        108 ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG- 166
               |                |: |     ||   :|: |     |||   :|  |: ||
Db        114 YC----------------ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT 153

Qy        167 ------------KTLSVS-------------QLELQDSG-----------------TWT 183
                         : ::||                 || ||                 |:
Db        154 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI 213

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              | |  | |    |:|       ||||||||||     ||||||||||||||||||||||
Db        214 CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 267

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 327

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 387

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 447

Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
```

```
Db        448 NHYTQKSLSLSPG 460


RESULT 44
AAW11639
ID   AAW11639 standard; protein; 475 AA.
XX
AC   AAW11639;
XX
DT   13-MAY-1997  (first entry)
XX
DE   Human anti-RSV monoclonal antibody RF-1 heavy chain.
XX
KW   Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus; RSV;
KW   fusion protein; F-protein; vaccine; immunotherapy; therapy;
KW   Epstein Barr virus; immortalisation; recombinant antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Leader_peptide
FT   Region          20. .49
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          50. .56
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          57. .70
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          71. .86
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          87. .118
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          119. .134
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          135. .145
FT                   /label= FR4
FT                   /note= "framework region 4"
FT   Region          146. .475
FT                   /label= Kappa
FT                   /note= "human gamma 1 constant region"
XX
PN   WO9640252-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US010070.
XX
PR   07-JUN-1995;   95US-00488376.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Brams P,  Chamat SS,  Pan L,  Walsh EE,  Heard CJ,  Newman RA;
XX
DR   WPI; 1997-099892/09.
DR   N-PSDB; AAT61241.
XX
PT   Human monoclonal antibody specific for respiratory syncytial virus fusion
PT   protein - used for the prevention and treatment of RSV infection.
XX
PS   Example 6; Fig 9b-c; 85pp; English.
XX
CC   A polypeptide (AAW11639) comprises a leader sequence, RF-1 heavy chain
CC   variable region (see also AAW11639), and human gamma 1 constant region.
CC   RF1 is a human monoclonal antibody (hMAb) specific for the fusion protein
CC   of respiratory syncytial virus (RSV). The polypeptide can be produced in
CC   eukaryotic host (e.g. CHO) cells transfected with vector NEOSPLA
CC   incorporating a DNA construct (AAT61241) including the RF-1 VH sequence.
CC   RF-1 and RF-2 heavy and light chains (see also AAW11638, AAW11640-41) are
CC   similarly produced. The transfected host cells provide a constant, stable
CC   supply of anti-RSV F-protein hMAbs for use in the treatment or prevention
CC   of RSV infection
XX
SQ   Sequence 475 AA;

  Query Match             47.4%;  Score 1280.5;  DB 2;  Length 475;
  Best Local Similarity   57.3%;  Pred. No. 3.4e-63;
  Matches  282;  Conservative   26;  Mismatches   87;  Indels   97;  Gaps   12;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--------------QKKSIQFHWK 54
              |: |    |      | :  |: |  :|: |||| |                    |       |
Db         10 LVAVATRVLSQVQLQESGPVVVKPTETLTLTCTVSGFSLSNPRMGVTWIRQPPGKALEW- 68

Qy         55 NSNQIKILGN-----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC 109
                  |||      : ||      |:|     |: ||         | : |:    |: || |
Db         69 -------LGNIFSSDEKSFSPSLKSRLTTSQDTSRS-----QVVLSLTNVDPVDTATYYC 116

Qy        110 EVEDQKEEVQLLVFGLTANSDTHL-LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
                  :: :: : |    :|   ||   :|: |     |||   :|  |:  ||
Db        117 --------ARVGLYDINAYYLYYLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA 168

Qy        167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||               || ||                    |: |
Db        169 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 228

Qy        185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
                |  | |     |:|        ||||||||||     ||||||||||||||||||||||
Db        229 NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 282

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 342

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 402

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 462

Qy        420 HYTQKSLSLSPG 431
              ||||||||||||
Db        463 HYTQKSLSLSPG 474


RESULT 45
ABG70743
ID   ABG70743 standard; protein; 473 AA.
XX
AC   ABG70743;
XX
DT   02-DEC-2002  (first entry)
XX
DE   Mouse/human chimeric anti-MAG antibody heavy chain protein.
XX
KW   Stroke; neurological disease; neurodegeneration; brain injury;
KW   spinal cord injury; chronic disease; Alzheimer's disease; tauopathy;
KW   fronto-temporal dementia; peripheral neuropathy; Parkinson's disease;
KW   Huntington's disease; multiple sclerosis; mouse; human; anti-MAG;
KW   antibody; heavy chain.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO200262383-A2.
XX
PD   15-AUG-2002.
XX
```

PF 08-FEB-2002; 2002WO-GB000551.
XX
PR 08-FEB-2001; 2001GB-00003174.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Irving EA, Vinson M;
XX
DR WPI; 2002-698554/75.
XX
PT Treating or preventing stroke and neurological diseases, e.g. Alzheimer's
PT disease, multiple sclerosis or Parkinson's disease, comprises
PT administering a myelin-associated glycoprotein (MAG) antagonist or anti-
PT MAG antibody.
XX
PS Disclosure; Fig 5; 41pp; English.
XX
CC The present invention relates to a new method of treating or preventing
CC stroke and other neurological diseases in a human. The method involves
CC administering a myelin-associated glycoprotein (MAG) antagonist or anti-
CC MAG antibody, including altered antibodies or their functional fragment.
CC The MAG antagonist or anti-MAG antibody, including altered antibodies or
CC their functional fragments are useful in preparing a medicament for
CC treating or preventing stroke and other neurological diseases, or for
CC inhibiting neurodegeneration and/or promoting functional recovery in a
CC human patient suffering or at risk of developing stroke or other
CC neurological disease, such as stroke, traumatic brain injury and spinal
CC cord injury, chronic diseases including Alzheimer's disease, fronto-
CC temporal dementias (tauopathies), peripheral neuropathy, Parkinson's
CC disease, Huntington's disease and multiple sclerosis. The present amino
CC acid sequence represents the mouse/human chimeric anti-MAG antibody heavy
CC chain protein
XX
SQ Sequence 473 AA;

Query Match 47.4%; Score 1280; DB 5; Length 473;
Best Local Similarity 58.3%; Pred. No. 3.7e-63;
Matches 281; Conservative 33; Mismatches 89; Indels 79; Gaps 14;

```
Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG--- 66
              |:   | | :     | :  | | |:| :::| ||      |   | | :|    :|
Db         10 LMAAAQSAEIQLVQSGPE--LKKPGETNKISCKAS---GYTFTNYNMNWVKQAPGKGLKW 64

Qy         67 ----SFLTKGPSKLND-RADSRRSLWDQGNFP-LIIKNLKIEDSDTYICEVEDQKEEVQL 120
                 :  |  |:  :| : :   ||    :   | | ||| ||: || |      :
Db         65 MGWINTYTGEPTYADDFKTNFAFSLETSASTAYLQISNLKNEDTATYFC------ARNPI 118

Qy        121 LVFGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------ 166
               :|:  | : :::   ||  ::|: |     |||   :|  |:  ||
Db        119 NYYGI--NYEGYVMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 176

Qy        167 -KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKVE 194
               : ::||                 || ||                 |: | |  | |
Db        177 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSN 234

Qy        195 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 249
               |:|       ||||||||||     ||| | ||||||||||||||||||||||||||
Db        235 TKVD----KKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVV 290

Qy        250 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 350

Qy        310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 410

Qy        370 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 470

Qy        430 PG 431
              ||
```

Db 471 PG 472

RESULT 46
AAW88464
ID AAW88464 standard; protein; 476 AA.
XX
AC AAW88464;
XX
DT 10-MAY-1999 (first entry)
XX
DE Monoclonal antibody 4B5 heavy chain variable region.
XX
KW Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
KW diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
KW lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
XX
OS Homo sapiens.
XX
PN WO9902545-A2.
XX
PD 21-JAN-1999.
XX
PF 08-JUL-1998; 98WO-IB001046.
XX
PR 08-JUL-1997; 97US-0051945P.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Dan MD;
XX
DR WPI; 1999-120769/10.
DR N-PSDB; AAX06951.
XX
PT New antibody 4B5 polynucleotides and polypeptides - used to develop
PT products for the diagnosis and treatment of cancers and for prophylactic
PT therapy to reduce risk of recurrence.
XX
PS Claim 1; Page 79-80; 83pp; English.
XX
CC This polypeptide comprises the heavy chain variable region of the
CC recombinant human monoclonal antibody (MAb) 4B5. 4B5 recognises
CC antibodies specific for GD2 antigen antibodies. Antibodies specific for
CC GD2 recognise various cancers including glioblastoma, neuroblastoma,
CC malignant and/or metastatic melanoma, breast adenocarcinoma, lung
CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
CC immunologic specificity for antibodies specific for GD2. These
CC derivatives, or antigen binding fragments, comprise regions of the 4B5
CC VDJ junction and regions spanning the 4B5 CDRs. Other derivatives include
CC Fab, F(ab')2, Fab', scFv and isolated heavy and light chains (see also
CC AAW88465). Polynucleotide fragments (see AAX06951-54) encoding 4B5
CC antibody V regions are also provided, and therapeutic plasmids and
CC vectors, including vaccinia virus vectors, comprising these
CC polynucleotides. 4B5 has been shown to mimic GD2, and is particularly
CC useful in generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g. astrocytoma,
CC oligodendroglioma, ependymoma, medulloblastoma, primitive neural
CC ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
CC large cell lung adenocarcinomas, squamous cell carcinoma,
CC bronchoalveoarcarcinoma, epithelial adenocarcinoma, and liver metastases,
CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
CC adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
CC uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
CC transitional squamous cell carcinoma of the bladder, B and T cell
CC lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma
XX
SQ Sequence 476 AA;

Query Match 47.4%; Score 1280; DB 2; Length 476;
Best Local Similarity 56.9%; Pred. No. 3.7e-63;
Matches 280; Conservative 27; Mismatches 91; Indels 94; Gaps 12;

```
Qy          11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFH-------------- 52
               :| |  |   | :|   |  |     | | :|:::| ||      |
Db           7 VLFLVAAATSARSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLNWVRQAPGQGLEW 66

Qy          53 --WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICE 110
                 | | |  |           |    |   |     |:   :  : : :  |: ||:  | |
Db          67 MGWMNPNSGK---------TGYAQKFQGRVTMTRNTSIRTAY-MELSGLRSEDTAVYFCA 116

Qy         111 VEDQKEEVQLL--VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-- 166
                 |: :   :|:        : ||  |:|: |     |||   :|  |:  ||
Db         117 RNADNVEMAAIYHYYGMD-------VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA 169

Qy         167 -----------KTLSVS-------------QLELQDSG-----------------TWTC 184
                        : ::||               || ||                    |: |
Db         170 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC 229

Qy         185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMIS 239
                 |  | |    |:|       ||||||||||     ||||||||||||||||||||||
Db         230 NV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 283

Qy         240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         284 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 343

Qy         300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         344 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 403

Qy         360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         404 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 463

Qy         420 HYTQKSLSLSPG 431
               ||||||||||||
Db         464 HYTQKSLSLSPG 475
```

RESULT 47
AAM49203
ID AAM49203 standard; protein; 448 AA.
XX
AC AAM49203;
XX
DT 29-AUG-2003 (revised)
DT 28-JUN-2002 (first entry)
XX
DE Humanised monoclonal antibody 5c8 (hu5c8) heavy chain.
XX
KW Monoclonal antibody; mAb; humanised; murine; mouse; 5c8; hu5c8;
KW heavy chain; anti-CD145; CD145-antibody complex; 3D structure;
KW three dimensional structure; drug design; drug discovery;
KW activated T cell; CD40 interaction; T cell dependent immune response;
KW agonist; antagonist; immune response; inflammatory response;
KW autoimmune disease; allergy; inhibitor response; organ graft rejection;
KW B cell cancer; Alzheimer's disease; multiple sclerosis; antiinflammatory;
KW immunosuppressive; antiallergic; cytostatic; dermatological;
KW antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic;
KW antiviral; antidiabetic; cardiant; antiischaemic; vasodilator;
KW antirheumatic; antiarthritic; antipsoriatic; immunomodulator; antibody;
KW complementarity determining region; CDR; protein co-ordinate data.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .219
FT /note= "Forms part of the crystal of the invention"
FT Region 31. .35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Binding-site 31. .33
FT /note= "Binds to CD145 (AAM49202)"
FT Region 50. .66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Binding-site 52
FT /note= "Binds to CD145 (AAM49202)"
FT Binding-site 54
FT /note= "Binds to CD145 (AAM49202)"
FT Binding-site 57
FT /note= "Binds to CD145 (AAM49202)"
FT Binding-site 59
FT /note= "Binds to CD145 (AAM49202)"
FT Region 99. .106
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT Binding-site 102. .103
FT /note= "Binds to CD145 (AAM49202)"
XX
PN WO200218445-A2.
XX
PD 07-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-US027352.
XX
PR 01-SEP-2000; 2000US-0229933P.
PR 16-MAR-2001; 2001US-0276452P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Karpusas M, Hsu Y, Taylor FR, Zheng Z;
XX
DR WPI; 2002-329760/36.
XX
PT Crystal comprising a CD154 polypeptide complexed with an anti-CD154
PT antibody, or its antigen binding fragment, useful for designing drugs for
PT the treatment of an autoimmune disease, an allergy, multiple sclerosis
PT and Alzheimer's disease.
XX
PS Example 1; Fig 8; 470pp; English.
XX
CC The invention relates to a crystal comprising a CD145 polypeptide in
CC complex with an anti-CD45 antibody or its antigen-binding fragment, and
CC the structure coordinates of such a crystal. In particular, the crystal
CC comprises human CD145 (AAM49202) and a humanised version of the murine
CC monoclonal antibody 5c8 (hu5c8; AAM49203, AAM49204). CD145, also known as
CC CD40L, gp39, T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type II
CC membrane glycoprotein which is transiently expressed on activated T
CC cells. It interacts with CD40 which is expressed on mature B cells,
CC macrophages, dendritic cells, fibroblasts and activated endothelial
CC cells. This CD40:CD145 interaction is required for T cell-dependent
CC antibody responses, type I T-helper cell responses, and nitric oxide (NO)
CC production by macrophages. NO mediates many of the pro-inflammatory
CC activities of macrophages, and disruption of the CD40:CD145 interaction
CC via the use of an anti-CD145 antibody has been shown to reduce the
CC symptoms of autoimmune and inflammatory conditions. The crystal structure
CC of the invention can be used to determine the three dimensional structure
CC of the CD145:anti-CD145 antibody complex, and thereby provide information
CC about this interaction which may be of use in designing non-antibody
CC CD145 agonists and antagonists which modulate the CD40:CD145 interaction.
CC Such compounds may be used in the treatment of an unwanted immune
CC response, an unwanted inflammatory response, an autoimmune disease, an
CC allergy, an inhibitor response to a therapeutic agent, rejection of a
CC donor organ, or a B cell cancer. They may be specifically be used to
CC treat systemic lupus erythematosus, lupus nephritis, lupus neuritis,
CC asthma, chronic obstructive pulmonary disease (COPD), bronchitis,
CC emphysema, multiple sclerosis, uveitis, Alzheimer's disease, traumatic
CC spinal cord injury, stroke, atherosclerosis, coronary restenosis,
CC ischaemic congestive heart failure, cirrhosis, hepatitis C, diabetic
CC nephropathy, glomerulonephritis, osteoarthritis, rheumatoid arthritis,
CC psoriasis, atopic dermatitis, systemic sclerosis, radiation-induced
CC fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma and
CC cachexia. Sequences AAM49203 and AAM49204 represent, respectively, the
CC heavy and light chains of the humanised version of the murine monoclonal

```
CC   antibody 5c8 (hu5c8). (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 448 AA;

  Query Match             47.4%;  Score 1279.5;  DB 5;  Length 448;
  Best Local Similarity   58.9%;  Pred. No. 3.7e-63;
  Matches  275;  Conservative   31;  Mismatches   74;  Indels   87;  Gaps   13;

Qy         25 GNKVVLGKKGDTVELTCTASQK--KSIQFHWKNSNQIKILGNQG-SFL-----TKGPSKL 76
              | :||  | | :|:|:| ||     |   :|     :|    ||  ::     : | :
Db          8 GAEVV--KPGASVKLSCKASGYIFTSYYMYW-----VKQAPGQGLEWIGEINPSNGDTNF 60

Qy         77 NDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
              |::  |: :|          : : :|: ||:  | |   | : ::
Db         61 NEKFKSKATLTVDKSASTAYMELSSLRSEDTAVYYCTRSDGRNDMD-------------- 106

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------- 172
               ||   :|: |     |||   :|  |:  ||              : ::||
Db        107 SWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 166

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                   || ||                   |: | |  | |    |:|       ||||
Db        167 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKS 220

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 280

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 340

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 400

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        401 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 447


RESULT 48
AAY30201
ID   AAY30201 standard; protein; 452 AA.
XX
AC   AAY30201;
XX
DT   17-OCT-2003  (revised)
DT   01-NOV-1999  (first entry)
XX
DE   Heavy chain sequence of chimeric anti-CD40 antibody chi220.
XX
KW   Heavy chain variable region; chimeric antibody; anti-CD40 antibody;
KW   chi220; humoral immune response; T cell dependent antigen;
KW   collagen induced arthritis; transplant induced rejection;
KW   T cell mediated disorder; autoimmune disease; inflammatory disease;
KW   transplantation.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO9942075-A2.
XX
PD   26-AUG-1999.
XX
PF   10-FEB-1999;   99WO-US002949.
XX
PR   19-FEB-1998;   98US-00026291.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Aruffo AA,  Hollenbaugh D,  Siadak AW,  Berry KK,  Harris LJ;
PI   Thorne BA,  Bajorath J,  Wu H,  Huse WD,  Watkins JD;
XX
DR   WPI; 1999-527408/44.
XX
PT   Antibody that binds human CD40, for treating T cell mediated disorders.
XX
PS   Claim 6; Page 20; 77pp; English.
XX
CC   The present sequence represents the heavy chain of a chimeric anti-CD40
CC   antibody designated chi220. The antibodies are effective in modulating
CC   humoral immune response against T cell dependent antigens, collagen
CC   induced arthritis and transplant induced rejection. They are also useful
CC   for their anti-inflammatory properties. The antibodies have wide
CC   therapeutic applications, including autoimmune and inflammatory diseases
CC   and transplantation. The antibody can be used in a pharmaceutical
CC   composition for treating a patient suffering from a T cell mediated
CC   disorder. They can also be used to treat autoimmune diseases,
CC   inflammatory diseases, and transplantation. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 452 AA;

  Query Match             47.4%;  Score 1279.5;  DB 2;  Length 452;
  Best Local Similarity   59.8%;  Pred. No. 3.7e-63;
  Matches  277;  Conservative   23;  Mismatches   80;  Indels   83;  Gaps   12;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD- 88
              | | |:|| ::| ||      |       :: :  :|    |    :|  :   : : |
Db         11 LKKPGETVRISCKAS---GYAFTTTGMQWVQEMPGKG---LKWIGWINTHSGVPKYVEDF 64

Qy         89 QGNFP-----------LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQ 137
              :| |             | | ||| ||: || | |         |  |            ||
Db         65 KGRFAFSLETSANTAYLQISNLKNEDTATYFC-VRSGNGNYDLAYFA---------YWGQ 114

Qy        138 SLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------------ 172
                :|: :     |||   :|  |:  ||              : ::||
Db        115 GTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 174

Qy        173 -QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT 213
                 || ||                   |: | |  | |    |:|       ||||||||
Db        175 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKT 228

Qy        214 HTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 268
              |||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 288

Qy        269 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 348

Qy        329 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 408

Qy        389 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        409 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 451


RESULT 49
AAY44721
ID   AAY44721 standard; protein; 470 AA.
XX
AC   AAY44721;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human immune system molecule, ISMO-2.
XX
KW   Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW   treatment; prevention; cell proliferation; immune system disorder.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .470
FT                   /label= Mature_ISMO-2
FT   Domain          34. .116
FT                   /note= "shows similarity to Ig superfamily protein
FT                   domain"
FT   Modified-site   47
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   69
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   81
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   92
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   98
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   105
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   120
FT                   /note= "N-glycosylated"
FT   Modified-site   142
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   154
FT                   /note= "Protein kinase C phosphorylation site"
FT   Domain          160. .225
FT                   /note= "shows similarity to Ig superfamily protein
FT                   domain"
FT   Modified-site   232
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   290
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   319
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   320
FT                   /note= "N-glycosylated"
FT   Modified-site   322
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   347
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   377
FT                   /note= "Casein kinase II phosphorylation site"
FT   Domain          383. .450
FT                   /note= "shows similarity to Ig superfamily protein
FT                   domain"
FT   Region          387. .409
FT                   /note= "conserved Ig/MHC protein block"
FT   Region          446. .463
FT                   /note= "conserved Ig/MHC protein block"
FT   Modified-site   460
FT                   /note= "Protein kinase C phosphorylation site"
XX
PN   WO200000608-A2.
XX
PD   06-JAN-2000.
XX
PF   21-JUN-1999;   99WO-US013995.
XX
PR   30-JUN-1998;   98US-00107223.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P,  Tang YT,  Corley NC,  Gorgone G,  Guegler KJ,  Patterson C;
PI   Baughn MR;
XX
DR   WPI; 2000-170916/15.
DR   N-PSDB; AAZ50012.
XX
PT   Immune system molecules used in the diagnosis, treatment and prevention
PT   of disorders associated with the immune system and cell proliferation.
XX
PS   Claim 1; Page 60-61; 69pp; English.
XX
CC   The present sequence is an immune system molecule, ISMO-2 from an Incyte
CC   clone 2849752 isolated from the human breast tumour cDNA library
CC   (BRSTTUT13). This sequence is expressed in several libraries, generally
CC   those associated with cancer, cell proliferation, immune response or
CC   trauma. It shows homology to vertebrate immunoglobulin gamma heavy-chain.
CC   The present sequence is useful in the diagnosis, treatment and prevention
CC   of disorders associated with the immune system and cell proliferation
XX
SQ   Sequence 470 AA;

  Query Match             47.3%;  Score 1279;  DB 3;  Length 470;
  Best Local Similarity   57.0%;  Pred. No. 4.1e-63;
  Matches  278;  Conservative   28;  Mismatches   98;  Indels   84;  Gaps   12;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61
              :||   | |   |         | :   | |  :|: |||| |      ::|   | |::
Db          2 KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIRSYYW---NWIRL 58

Qy         62 LGNQ-----GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVED 113
                :      |   | | :  |    || ::     :  | | : ::   |:  | |
Db         59 PPGKGLEWIGYIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARPP 118

Qy        114 QKEEVQLLVFGLTANSDTHLLQG-QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------ 166
                        | : |    | :   :|: |     |||   :|  |:  ||
Db        119 P-----------NATTTTVWTSGAKGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC 167

Qy        167 -------KTLSVS-------------QLELQDSG------------------TWTCTVLQ 188
                    : ::||               || ||                    |: | |
Db        168 LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV-- 225

Qy        189 NQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE 243
              | |    |:|       ||||||||||     ||||||||||||||||||||||||||
Db        226 NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 281

Qy        244 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 341

Qy        304 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 401

Qy        364 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        402 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQ 461

Qy        424 KSLSLSPG 431
              ||||||||
Db        462 KSLSLSPG 469


RESULT 50
ADD25783
ID   ADD25783 standard; protein; 492 AA.
XX
AC   ADD25783;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated protein #157.
XX
KW   Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
```

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XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 344; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 492 AA;

  Query Match             47.3%;  Score 1279;  DB 7;  Length 492;
  Best Local Similarity   55.8%;  Pred. No. 4.3e-63;
  Matches  279;  Conservative   33;  Mismatches   92;  Indels   96;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |:|||      :||        ||    :     |: | :|| ||    |  : ::  :
Db         19 MSRGVD-----IVL--------TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS--- 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE--------- 110
                 |           |||     :| |    | :: | |   :: ||: || |:
Db         63 --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120

Qy        111 -----VEDQK-------------EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                  :| ::               :|||    |       |  |   ||| |:     :|
Db        121 GSGTKLEIKRGGGGSGGGGSGGGGSQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD 177

Qy        152 SVQ-CRSPRGKNIQ--------GGKT--------------------LSVSQLELQDSGT 181
                |   | | || ::        ||                      | :: |:  |:
Db        178 GVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM 237

Qy        182 WTCTVLQNQKKVEFK-----IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPK 231
                : |       :: |      : :       ||||||||||     ||||||||||||||
Db        238 YYCA------RIHFDYWGQGVMVTVSSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 291

Qy        232 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 351

Qy        292 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 411

Qy        352 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 471

Qy        412 VMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||
Db        472 VMHEALHNHYTQKSLSLSPG 491


RESULT 51
AAB81972
ID   AAB81972 standard; protein; 581 AA.
XX
AC   AAB81972;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
XX
KW   Ganglioside; GD2; complementation determining region; CDR; antibody;
KW   mouse; cancer.
XX
OS   Synthetic.
XX
PN   WO200123573-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006773.
XX
PR   30-SEP-1999;   99JP-00278290.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266163/27.
XX
PT   Human type complementation-determining domain transplanted antibody and
PT   derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT   e.g. tumors, has low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Example 3; Page 111-114; 123pp; Japanese.
XX
CC   The present invention describes an antibody, which can react specifically
CC   with ganglioside GD2, and is transplanted with a human type
CC   complementation-determining domain (CDR), or its fragments. The antibody
```

```
CC   and its derivatives are useful in diagnosis and therapy of tumours,
CC   particularly cancer diagnosis. The present sequence is a protein used in
CC   the exemplification of the invention
XX
SQ   Sequence 581 AA;

  Query Match             47.3%;  Score 1278.5;  DB 4;  Length 581;
  Best Local Similarity   57.7%;  Pred. No. 5.5e-63;
  Matches  275;  Conservative   25;  Mismatches   96;  Indels   81;  Gaps   10;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL- 86
              | |   |: :||| |      |   ||      | |   |      | :  |    || ::
Db         11 LVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLTIS 70

Qy         87 WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
              |     : :|   :  :|| :     : ::      :            ||   :|: |
Db         71 KDNSKNQVFLKMSSLTAADTAVYYCAKRSDDYSWFAY----------WGQGTLVTVSSA 119

Qy        147 PGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG 180
                |||   :|  |:  ||              : ::||                || ||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 ------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----P 217
                              |: | |  | |    |:|       ||||||||||      |
Db        180 LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAP 233

Qy        218 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 293

Qy        278 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 353

Qy        338 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 413

Qy        398 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------------LQLDETCAEAQ 442
              |||||||||||||||||||||||||||||||||          |||:    : |
Db        414 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQ 470


RESULT 52
ADD25784
ID   ADD25784 standard; protein; 543 AA.
XX
AC   ADD25784;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated protein #158.
XX
KW   Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 345; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 543 AA;

  Query Match             47.3%;  Score 1277;  DB 7;  Length 543;
  Best Local Similarity   55.8%;  Pred. No. 6.2e-63;
  Matches  279;  Conservative   33;  Mismatches   92;  Indels   96;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |:|||      :||         ||    :    |: | :|| ||   |  : ::  :
Db         19 MSRGVD-----IVL--------TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS--- 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE--------- 110
                |      |||     :| |    | :: | |  :: ||: || |:
Db         63 --GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF 120

Qy        111 -----VEDQK-------------EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                  :| ::               :|||   |      |  |   ||| |:     :|
Db        121 GSGTKLEIKRGGGGSGGGGSGGGGSQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD 177

Qy        152 SVQ-CRSPRGKNIQ--------GGKT--------------------LSVSQLELQDSGT 181
```

```
                |   | | || ::       ||                          | :: |:  |:
Db        178 GVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLKINSLQTDDTAM 237

Qy        182 WTCTVLQNQKKVEFK-----IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPPK 231
              : |       :: |      : :      ||||||||||     ||||||||||||||
Db        238 YYCA------RIHFDYWGQGVMVTVSSDLEPKSCDKTHTCPPCPAPELLGGPSVFLFPPPK 291

Qy        232 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 351

Qy        292 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 411

Qy        352 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 471

Qy        412 VMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||
Db        472 VMHEALHNHYTQKSLSLSPG 491
```

RESULT 53
ABR39847
ID ABR39847 standard; protein; 461 AA.
XX
AC ABR39847;
XX
DT 18-AUG-2003 (first entry)
XX
DE Hu266 N56S heavy chain.
XX
KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW immunostimulant.
XX
OS Homo sapiens.
XX
PN WO2003016466-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US021322.
XX
PR 17-AUG-2001; 2001US-0313224P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Jia AY, Tsurushita N, Vasquez MJ;
XX
DR WPI; 2003-278557/27.
DR N-PSDB; ACC47231.
XX
PT New antibodies comprising a heavy chain and a light chain complementarity
PT determining regions from antibody 266, for treating and preventing
PT conditions associated with the A beta peptide, e.g. Alzheimer's disease
PT or Down syndrome.
XX
PS Disclosure; Fig 6; 82pp; English.
XX
CC The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
CC 266. The antibodies are useful for treating and preventing conditions
CC associated with the Abeta peptide, such as Alzheimer's disease, Down
CC syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
CC humans; for determining whether a human subject will respond to treatment
CC using humanized antibodies against Abeta; for treating, preventing and
CC reversing cognitive decline in clinical or pre-clinical Alzheimer's
CC disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting
CC formation of amyloid plaques of the effects of toxic soluble Abeta
CC species in humans. Treatment of the patients with antibody will inhibit
CC or prevent cognitive decline typically associated with disease
CC progression and reverses it. The present sequence represents a humanised
CC anti-Abeta antibody 266 N56S heavy chain
XX
SQ Sequence 461 AA;

```
  Query Match             47.2%;  Score 1275.5;  DB 6;  Length 461;
  Best Local Similarity   57.0%;  Pred. No. 6.3e-63;
  Matches  281;  Conservative   31;  Mismatches   86;  Indels   95;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS-- 56
              || |:    |:|||:  |       :   | : | :: |:| ||         |
Db          1 MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP 60

Qy         57 -------NQIKILGNQGSF--LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTY 107
                    ||  :|:   :    ||   :: | ::: :|: | |      :|: ||:  |
Db         61 GKGLELVAQINSVGSSTYYPDTVKGRFTIS-RDNAKNTLYLQMN------SLRAEDTAVY 113

Qy        108 ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG- 166
              |                |: |      ||   :|: |     |||   :|  |:  ||
Db        114 YC----------------ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT 153

Qy        167 ------------KTLSVS-------------QLELQDSG-----------------TWT 183
                         : ::||              || ||                    |:
Db        154 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI 213

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              | |  | |    |:|       ||||||||||     ||||||||||||||||||||
Db        214 CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 267

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 327

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 387

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 447

Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
Db        448 NHYTQKSLSLSPG 460
```

RESULT 54
ABR39843
ID ABR39843 standard; protein; 461 AA.
XX
AC ABR39843;
XX
DT 18-AUG-2003 (first entry)
XX
DE Hu266 N56S heavy chain.
XX
KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW immunostimulant.
XX
OS Homo sapiens.
XX
PN WO2003016466-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US021322.
XX
PR 17-AUG-2001; 2001US-0313224P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Jia AY, Tsurushita N, Vasquez MJ;
XX
DR WPI; 2003-278557/27.

```
DR   N-PSDB; ACC47227.
XX
PT   New antibodies comprising a heavy chain and a light chain complementarity
PT   determining regions from antibody 266, for treating and preventing
PT   conditions associated with the A beta peptide, e.g. Alzheimer's disease
PT   or Down syndrome.
XX
PS   Disclosure; Fig 2; 82pp; English.
XX
CC   The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
CC   266. The antibodies are useful for treating and preventing conditions
CC   associated with the Abeta peptide, such as Alzheimer's disease, Down
CC   syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
CC   humans; for determining whether a human subject will respond to treatment
CC   using humanized antibodies against Abeta; for treating, preventing and
CC   reversing cognitive decline in clinical or pre-clinical Alzheimer's
CC   disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting
CC   formation of amyloid plaques of the effects of toxic soluble Abeta
CC   species in humans. Treatment of the patients with antibody will inhibit
CC   or prevent cognitive decline typically associated with disease
CC   progression and reverses it. The present sequence represents a humanised
CC   anti-Abeta antibody 266 N56S heavy chain
XX
SQ   Sequence 461 AA;

  Query Match             47.2%;  Score 1275.5;  DB 6;  Length 461;
  Best Local Similarity   57.0%;  Pred. No. 6.3e-63;
  Matches  281;  Conservative   31;  Mismatches   86;  Indels   95;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS-- 56
              || |:    |:|||:  |       :   | : | :: |:| ||        |
Db          1 MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP 60

Qy         57 -------NQIKILGNQGSF--LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTY 107
                   ||  :|:   :    ||   :: | ::: :|: | |       :|: ||:  |
Db         61 GKGLELVAQINSVGSSTYYPDTVKGRFTIS-RDNAKNTLYLQMN------SLRAEDTAVY 113

Qy        108 ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG- 166
               |              |: |     ||   :|: |     |||   :|  |:  ||
Db        114 YC----------------ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT 153

Qy        167 ------------KTLSVS-------------QLELQDSG-----------------TWT 183
                       : ::||                  || ||                  |:
Db        154 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI 213

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              | |  | |     |:|       ||||||||||     ||||||||||||||||||||
Db        214 CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 267

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 327

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 387

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 447

Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
Db        448 NHYTQKSLSLSPG 460


RESULT 55
AAE33444
ID   AAE33444 standard; protein; 579 AA.
XX
AC   AAE33444;
XX
DT   02-APR-2003  (first entry)
XX
DE   KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX
KW   Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EpCAM;
KW   cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX
OS   Unidentified.
XX
PN   WO200290566-A2.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-US013844.
XX
PR   03-MAY-2001; 2001US-0288564P.
XX
PA   (LEXI-) LEXIGEN PHARM CORP.
XX
PI   Gillies SD,  Lo K,  Qian X;
XX
DR   WPI; 2003-111985/10.
DR   N-PSDB; AAD51139.
XX
PT   New recombinant anti-EpCAM antibody having an amino acid sequence
PT   defining an immunoglobulin light or heavy chain framework region, useful
PT   for the diagnosis, prognosis and treatment of cancer.
XX
PS   Disclosure; Page 80-82; 82pp; English.
XX
CC   The present invention relates to novel recombinant anti-EpCAM (human
CC   epithelial cell adhesion molecule) antibodies comprising an amino acid
CC   sequence defining an immunoglobulin light or heavy chain framework
CC   region. Sequences of the present invention are useful for the diagnosis,
CC   prognosis and treatment of cancer. They are also used in gene therapy.
CC   The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC   fusion protein. This sequence is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 579 AA;

  Query Match             47.2%;  Score 1275.5;  DB 6;  Length 579;
  Best Local Similarity   57.7%;  Pred. No. 8e-63;
  Matches  281;  Conservative   29;  Mismatches   70;  Indels  107;  Gaps   14;

Qy         32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLW 87
              | |:||:::| ||      :  :|       | |    |  :  |  |:  :|
Db         13 KPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTYADD--------- 63

Qy         88 DQGNFP----------LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              :| |             | | ||: ||: || |         |: :  |        :  ||
Db         64 FKGRFAFSLETSTSTAFLQINNLRSEDTATYFC--------VRFISKG------DYWGQG 109

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS----------- 172
              |:|::  |  |  |||   :|  |:  ||             : ::||
Db        110 TSVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 167

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |    |:|       |||||||
Db        168 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK 221

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 281

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 341

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        342 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 401

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------------LQLD 435
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                ||||||||||||||||||||||||||||||||||||||||||||            |||:
Db        402 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLE 461

Qy        436 ETCAEAQ 442
                  : |
Db        462 HLLLDLQ 468

RESULT 56
AAW86003
ID   AAW86003 standard; protein; 595 AA.
XX
AC   AAW86003;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Anti-5T4 single chain antibody 5T4Sab1.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; mouse; human; 5T4Sab1.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
DR   N-PSDB; AAV80291.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 1; Fig 1B; 82pp; English.
XX
CC   This is the amino acid sequence of a single chain antibody (Sab), termed
CC   5T4Sab1, comprising an scFv derived from murine monoclonal antibody 5T4
CC   (see AAW86002) and the human g1 constant region. cDNA (see AAV80291)
CC   encoding the Sab has been inserted into vector pCIneo to allow expression
CC   in mammalian cells. The trophoblast cell surface antigen defined by 5T4
CC   is expressed at high levels on the cells of a wide variety of human
CC   tumours. The invention relates to a vector comprising a nucleotide
CC   sequence coding for a tumour interacting protein (TIP) and optionally a
CC   nucleotide sequence of interest (NOI) which encodes a protein of interest
CC   (POI), the vector being capable of delivering the NOI and/or POI to the
CC   tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The
CC   vector is used to treat cancer, and may also used as a gene delivery
CC   system for introducing at least 1 gene encoding a TIP (preferably a
CC   tumour binding protein) into a haematopoietic cell lineage
XX
SQ   Sequence 595 AA;

  Query Match             47.2%;  Score 1275;  DB 2;  Length 595;
  Best Local Similarity   59.4%;  Pred. No. 8.8e-63;
  Matches  277;  Conservative   18;  Mismatches   81;  Indels   90;  Gaps   11;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              ||   :|  || | :|| |||  |    |                    : |: |    |
Db        162 TQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKP-----------GQSPTLLISYTSS 210

Qy         83 R-RSLWDQ-------GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL 134
              |  : |:        :|   |  |: ||   | |: :                    ||
Db        211 RYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQD-------------YNSPPTFG 256

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS--------- 172
               |  | :    |  |  |||   :|  |:  ||                 :  ::||
Db        257 GGTKLEIKRASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 314

Qy        173 ----QLELQDSG------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                     || ||                 |: |  |   | |   |:|     ||||
Db        315 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 368

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
              ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 428

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 488

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 548

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        549 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 594

RESULT 57
AAO31101
ID   AAO31101 standard; protein; 445 AA.
XX
AC   AAO31101;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human A2-G8 SCF antibody heavy chain variable and constant region.
XX
KW   Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
KW   steel factor; c-kit ligand; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003051311-A2.
XX
PD   26-JUN-2003.
XX
PF   16-DEC-2002; 2002WO-US040227.
XX
PR   17-DEC-2001; 2001US-0342174P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Takeuchi T,  Tomkinson A,  Neben S;
XX
DR   WPI; 2003-523500/49.
XX
PT   New purified human antibody that binds to stem cell factor protein,
PT   useful for preparing a composition for treating asthma.
XX
PS   Claim 9; Page 47; 94pp; English.
XX
CC   The invention provides human antibodies that bind to stem cell factor
CC   (SCF) protein. SCF is also known as mast cell growth factor, steel factor
CC   or c-kit ligand. Antibodies of the invention are useful for preparing
CC   compositions for treating asthma. They are also used in gene therapy. The
CC   present sequence is human SCF antibody heavy chain variable and constant
CC   region
XX
SQ   Sequence 445 AA;
```

```
  Query Match             47.2%;  Score 1274.5;  DB 6;  Length 445;
  Best Local Similarity   59.2%;  Pred. No. 6.9e-63;
  Matches  277;  Conservative   27;  Mismatches   67;  Indels   97;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFL----TKG 72
              | : | :: |:| ||              |       | ::    | |: ||      ||
Db          8 LVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA----ISGSGGSTYYADSVKG 63

Qy         73 PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH 132
                :: | :|: :|: | |      :|: ||:  | |   |           |: |
Db         64 RFTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCARRD----------FFAHFD-- 103

Qy        133 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------- 172
               : ||   :|: |     |||   :|  |:  ||             : ::||
Db        104 -VWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 162

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                   || ||                   |: | |  | |    |:|       |||
Db        163 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 216

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        217 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 276

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 336

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 396

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 444


RESULT 58
ABR39844
ID   ABR39844 standard; protein; 461 AA.
XX
AC   ABR39844;
XX
DT   18-AUG-2003  (first entry)
XX
DE   Hu266 N56T heavy chain.
XX
KW   Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW   immunostimulant.
XX
OS   Homo sapiens.
XX
PN   WO2003016466-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US021322.
XX
PR   17-AUG-2001; 2001US-0313224P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Jia AY,  Tsurushita N,  Vasquez MJ;
XX
DR   WPI; 2003-278557/27.
DR   N-PSDB; ACC47228.
XX
PT   New antibodies comprising a heavy chain and a light chain complementarity
PT   determining regions from antibody 266, for treating and preventing
PT   conditions associated with the A beta peptide, e.g. Alzheimer's disease
PT   or Down syndrome.
XX
PS   Disclosure; Fig 3; 82pp; English.
XX
CC   The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
CC   266. The antibodies are useful for treating and preventing conditions
CC   associated with the Abeta peptide, such as Alzheimer's disease, Down
CC   syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
CC   humans; for determining whether a human subject will respond to treatment
CC   using humanized antibodies against Abeta; for treating, preventing and
CC   reversing cognitive decline in clinical or pre-clinical Alzheimer's
CC   disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting
CC   formation of amyloid plaques of the effects of toxic soluble Abeta
CC   species in humans. Treatment of the patients with antibody will inhibit
CC   or prevent cognitive decline typically associated with disease
CC   progression and reverses it. The present sequence represents a humanised
CC   anti-Abeta antibody 266 N56T heavy chain
XX
SQ   Sequence 461 AA;

  Query Match             47.2%;  Score 1274.5;  DB 6;  Length 461;
  Best Local Similarity   57.0%;  Pred. No. 7.2e-63;
  Matches  281;  Conservative   30;  Mismatches   87;  Indels   95;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS-- 56
              || |:    |:|||:  |       :   | : | :: |:| ||          |
Db          1 MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP 60

Qy         57 -------NQIKILGNQGSF--LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTY 107
                    ||  :|   :    ||   :: | ::: :|: | |      :|: ||:  |
Db         61 GKGLELVAQINSVGTSTYYPDTVKGRFTIS-RDNAKNTLYLQMN------SLRAEDTAVY 113

Qy        108 ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG- 166
              |                  |: |     ||   :|: |     |||   :|  |:  ||
Db        114 YC-----------------ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT 153

Qy        167 ------------KTLSVS-------------QLELQDSG------------------TWT 183
                         : ::||                 || ||                  |:
Db        154 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI 213

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              | |  | |    |:|       ||||||||||     ||||||||||||||||||||
Db        214 CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 267

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 327

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 387

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 447

Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
Db        448 NHYTQKSLSLSPG 460


RESULT 59
ABR39848
ID   ABR39848 standard; protein; 461 AA.
XX
AC   ABR39848;
XX
DT   18-AUG-2003  (first entry)
XX
DE   Hu266 N56T heavy chain.
XX
KW   Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW   immunostimulant.
XX
OS   Homo sapiens.
XX
```

```
PN   WO2003016466-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US021322.
XX
PR   17-AUG-2001; 2001US-0313224P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Jia AY,  Tsurushita N,  Vasquez MJ;
XX
DR   WPI; 2003-278557/27.
DR   N-PSDB; ACC47232.
XX
PT   New antibodies comprising a heavy chain and a light chain complementarity
PT   determining regions from antibody 266, for treating and preventing
PT   conditions associated with the A beta peptide, e.g. Alzheimer's disease
PT   or Down syndrome.
XX
PS   Disclosure; Fig 7; 82pp; English.
XX
CC   The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
CC   266. The antibodies are useful for treating and preventing conditions
CC   associated with the Abeta peptide, such as Alzheimer's disease, Down
CC   syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
CC   humans; for determining whether a human subject will respond to treatment
CC   using humanized antibodies against Abeta; for treating, preventing and
CC   reversing cognitive decline in clinical or pre-clinical Alzheimer's
CC   disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting
CC   formation of amyloid plaques of the effects of toxic soluble Abeta
CC   species in humans. Treatment of the patients with antibody will inhibit
CC   or prevent cognitive decline typically associated with disease
CC   progression and reverses it. The present sequence represents a humanised
CC   anti-Abeta antibody 266 N56T heavy chain
XX
SQ   Sequence 461 AA;

  Query Match             47.2%;  Score 1274.5;  DB 6;  Length 461;
  Best Local Similarity   57.0%;  Pred. No. 7.2e-63;
  Matches  281;  Conservative   30;  Mismatches   87;  Indels   95;  Gaps   13;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS-- 56
              || |:    |:|||:  |       :   | : | :: |:| ||           |
Db          1 MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP 60

Qy         57 -------NQIKILGNQGSF--LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTY 107
                   ||  :|   :    ||   :: | ::: :|: | |      :|: ||:  |
Db         61 GKGLELVAQINSVGTSTYYPDTVKGRFTIS-RDNAKNTLYLQMN------SLRAEDTAVY 113

Qy        108 ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG- 166
               |                |: |     ||   :|: |     |||   :|  |:  ||
Db        114 YC----------------ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT 153

Qy        167 ------------KTLSVS-------------QLELQDSG-----------------TWT 183
                         : ::||               || ||                 |:
Db        154 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI 213

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI 238
              | |  | |    |:|       ||||||||||     ||||||||||||||||||||||
Db        214 CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 267

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 327

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 387

Qy        359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 447

Qy        419 NHYTQKSLSLSPG 431
              |||||||||||||
Db        448 NHYTQKSLSLSPG 460


RESULT 60
AAB36206
ID   AAB36206 standard; protein; 473 AA.
XX
AC   AAB36206;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human immune system associated protein HISAP-4.
XX
KW   Human; immune system associated protein; HISAP-4; immune disorder;
KW   infection; autoimmune disease; cancer.
XX
OS   Homo sapiens.
XX
PN   US6135941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998;   98US-00049672.
XX
PR   27-MAR-1998;   98US-00049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT,  Yue H,  Lal P,  Corley NC,  Guegler KJ,  Baughn MR;
PI   Hillman JL,  Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   N-PSDB; AAC66522.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing immune
PT   or cell proliferative disorders or infections.
XX
PS   Claim 1; Col 53-56; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ   Sequence 473 AA;

  Query Match             47.2%;  Score 1274.5;  DB 4;  Length 473;
  Best Local Similarity   57.2%;  Pred. No. 7.4e-63;
  Matches  278;  Conservative   29;  Mismatches  102;  Indels   77;  Gaps   11;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQI 59
              :||   | |  |          | :   | |  :|: |||  |    |  ::|    |
Db          2 KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQP 61

Qy         60 KILGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQ 114
                  | :  |     | :  |    || ::     :  | | : ::   |:  | |  :|
Db         62 PGKGLEWIGYIYYSGSTLYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDD- 120

Qy        115 KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------- 166
                        ||   :    : ||   :|: |     |||   :|  |:  ||
Db        121 --------VGLRGGNYGMDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV 172

Qy        167 -----KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQ 190
                  : ::||               || ||                 |: | |  |
Db        173 KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NH 230
```

```
Qy        191 KKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
              |    |:|       |||||||||||     |||||||||||||||||||||||||||||
Db        231 KPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 286

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 346

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
              |||||||||||||||||||||||||||||||||||:|:||||||||||||||||||||||
Db        347 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE 406

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 466

Qy        426 LSLSPG 431
              ||||||
Db        467 LSLSPG 472
```

RESULT 61
AAE27928
ID   AAE27928 standard; protein; 468 AA.
XX
AC   AAE27928;
XX
DT   27-DEC-2002 (first entry)
XX
DE   Human C5E10 antibody heavy chain protein.
XX
KW   Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW   neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW   non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200260955-A2.
XX
PD   08-AUG-2002.
XX
PF   29-JAN-2002; 2002WO-US002373.
XX
PR   29-JAN-2001; 2001US-0264318P.
PR   16-NOV-2001; 2001US-0331481P.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Braslawsky GR, Hanna N, Chinn P;
XX
DR   WPI; 2002-698547/75.
DR   N-PSDB; AAD45757.
XX
PT   Novel domain deleted CC49 antibody reactive with tumor associated antigen
PT   -72, or C2B8 antibody reactive with CD20, useful for treating
PT   myelosuppressed patient suffering from a neoplastic disorder.
XX
PS   Example 3; Fig 6A; 74pp; English.
XX
CC   The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC   Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC   deleted sequence in which CH2 domain has been deleted and are reactive
CC   with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC   with CD20 and comprise a heavy chain having a sequence of a derived
CC   domain deleted C2B8 construct where the CH2 domain has been deleted.
CC   Sequences of the invention are useful for imaging a neoplasm. They are
CC   also useful for treating myelosuppressed patients suffering from
CC   neoplastic disorder such as haematologic neoplasm, preferably non-
CC   Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC   neoplastic disorder, colon cancer and haematologic malignancy. They are
CC   useful for reducing tumour size, inhibiting tumour growth and/or
CC   prolonging the survival time of tumour-bearing animals and for treating
CC   tumours. The present sequence is human C5E10 heavy chain protein. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 468 AA;

```
  Query Match             47.2%;  Score 1274;  DB 5;  Length 468;
  Best Local Similarity   58.0%;  Pred. No. 7.8e-63;
  Matches  280;  Conservative   28;  Mismatches   95;  Indels   80;  Gaps   13;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKG-------DTVELTCTASQKKSIQF--HWKNSNQIK 60
              | |:  |    |:    ::| | : |          :: :||| |       :  :|    |
Db          4 LALLFCLVTFPSCIL-SQVQLKESGPGLVAPSQSLSITCTVSGFSLTDYGVNWVRQPPGK 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIK--NLKIEDSDTYICEVEDQKEE 117
              |    |      |  :  |      || |:  |      : :|   :|: :|:   | |
Db         63 GLEWLGMIWDNGRTDYNSALKSRLSINKDNSKSQVFLKMTSLQTDDTARYYC-------- 114

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG----------- 166
               :|  :   |       ||  |||: |      |||    :|   |:  ||
Db        115 -ARCYYGSSPYFD---YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 170

Qy        167 --KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKV 193
                : ::||              || ||                  |: |  |  |  |
Db        171 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 228

Qy        194 EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
                |:|       |||||||||||     |||||||||||||||||||||||||||||||
Db        229 NTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 284

Qy        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 344

Qy        309 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 404

Qy        369 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 464

Qy        429 SPG 431
              |||
Db        465 SPG 467
```

RESULT 62
ABB82837
ID   ABB82837 standard; protein; 468 AA.
XX
AC   ABB82837;
XX
DT   31-MAR-2003 (first entry)
XX
DE   Antibody C5E10 heavy chain.
XX
KW   C5E10; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW   vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW   thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
KW   neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW   dermatological; immunosuppressive; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO200296948-A2.
XX
PD   05-DEC-2002.
XX
PF   29-JAN-2002; 2002WO-US002374.
XX
PR   29-JAN-2001; 2001US-0264318P.
PR   16-NOV-2001; 2001US-0331481P.
PR   21-DEC-2001; 2001US-0341858P.

```
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Braslawsky GR,  Hanna N,  Chinn P,  Hariharan K;
XX
DR   WPI; 2003-140446/13.
DR   N-PSDB; ABZ24021.
XX
PT   Novel dimeric antibody useful for treating immune disorder and neoplastic
PT   disorder, has several non-covalently associated monomeric subunits.
XX
PS   Example 3; Fig 6; 78pp; English.
XX
CC   The invention relates to a dimeric antibody (I) comprising several
CC   monomeric subunits, where the monomeric subunits are non-covalently
CC   associated. (I) is useful for treating a disorder, especially immune
CC   disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC   resistant Hodgkin's disease high grade, low grade and intermediate grade
CC   non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC   lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC   lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC   AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC   lymphoadenopathy, small lymphocytic, follicular, diffuse large cell,
CC   diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC   small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC   cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC   detailed description of the various uses of (I)). The present sequence
CC   represents the antibody C5E10 heavy chain
XX
SQ   Sequence 468 AA;

  Query Match             47.2%;  Score 1274;  DB 6;  Length 468;
  Best Local Similarity   58.0%;  Pred. No. 7.8e-63;
  Matches  280;  Conservative   28;  Mismatches   95;  Indels   80;  Gaps   13;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKG-------DTVELTCTASQKKSIQF--HWKNSNQIK 60
Db          4 LALLFCLVTFPSCIL-SQVQLKESGPGLVAPSQSLSITCTVSGFSLTDYGVNWVRQPPGK 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIK--NLKIEDSDTYICEVEDQKEE 117
Db         63 GLEWLGMIWDNGRTDYNSALKSRLSINKDNSKSQVFLKMTSLQTDDTARYYC-------- 114

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
Db        115 -ARCYYGSSPYFD---YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 170

Qy        167 --KTLSVS------------QLELQDSG-----------------TWTCTVLQNQKKV 193
Db        171 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 228

Qy        194 EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
Db        229 NTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 284

Qy        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
Db        285 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 344

Qy        309 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 368
Db        345 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 404

Qy        369 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
Db        405 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 464

Qy        429 SPG 431
Db        465 SPG 467

RESULT 63

AAE35327
ID   AAE35327 standard; protein; 444 AA.
XX
AC   AAE35327;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Humanised murine antibody BIWA4 heavy chain protein.
XX
KW   CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease;
KW   antigen; cytostatic; BIWA4 antibody; murine.
XX
OS   Homo sapiens.
XX
PN   EP1258255-A1.
XX
PD   20-NOV-2002.
XX
PF   18-MAY-2001; 2001EP-00112227.
XX
PR   18-MAY-2001; 2001EP-00112227.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI   Adolf G,  Heider K,  Patzelt E,  Sproll M;
XX
DR   WPI; 2003-177273/18.
DR   N-PSDB; AAD53977.
XX
PT   New compound useful for treatment of cancer comprises CD44 specific
PT   antibody molecule conjugated to a highly cytotoxic drug, which cleaves
PT   under intracellular conditions.
XX
PS   Claim 7; Page 15-16; 31pp; English.
XX
CC   The invention relates to a compound comprising CD44 specific antibody
CC   molecule conjugated to a highly cytotoxic drug, which cleaves under
CC   intracellular conditions. The compound is used in pharmaceutical
CC   composition for the treatment of cancer, solid tumours, and as an
CC   adjuvant to surgical intervention to treat minimal residual disease. The
CC   present sequence is humanised murine antibody BIWA4 heavy chain protein
CC   used in the invention
XX
SQ   Sequence 444 AA;

  Query Match             47.1%;  Score 1273.5;  DB 6;  Length 444;
  Best Local Similarity   59.3%;  Pred. No. 7.8e-63;
  Matches  275;  Conservative   27;  Mismatches   69;  Indels   93;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFL-----TKGPSKL 76
Db         11 LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
Db         71 S-RDNAKNSLYLQMN------SLRAEDTAVYYCARQ-----------GLD-------YWG 105

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS----------- 172
Db        106 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 165

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
Db        166 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 219

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
Db        220 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 279

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
Db        280 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 339
```

```
Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 399

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        400 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443


RESULT 64
AAE34876
ID   AAE34876 standard; protein; 444 AA.
XX
AC   AAE34876;
XX
DT   28-MAY-2003  (first entry)
XX
DE   BIWA4/8 antibody heavy chain mature protein.
XX
KW   BIWA8 antibody; heavy chain variable region; light chain variable region;
KW   VH; VL; CD44v6; medicament; cancer; antibody therapy.
XX
OS   Unidentified.
XX
PN   WO200294879-A1.
XX
PD   28-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-EP005467.
XX
PR   18-MAY-2001; 2001EP-00112237.
PR   26-SEP-2001; 2001US-0325147P.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI   Adolf G,  Ostermann E,  Patzelt E,  Sproll M,  Heider K;
PI   Miglietta JJ,  Van Dongen AAMS;
XX
DR   WPI; 2003-129413/12.
DR   N-PSDB; AAD53212, AAD53215.
XX
PT   New antibodies specific for an epitope coded by the variant exon of the
PT   CD44 gene, useful for treating cancer, including non-small cell lung,
PT   breast, head and neck, ovarian and lung cancer.
XX
PS   Claim 24; Col 44; 78pp; English.
XX
CC   The present invention relates to novel antibody molecules comprising a
CC   variable region of the heavy (VH) and/or light chain (VL) of CD44v6
CC   specific humanised antibody called BIWA8 and BIWA4. Sequences of the
CC   invention are useful for manufacturing a medicament and for treating
CC   cancer including colorectum, non-small cell lung, breast, head and neck,
CC   ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
CC   brain. They are also useful in antibody therapy. The present sequence is
CC   BIWA4/8 antibody heavy chain mature protein. This sequence is used in the
CC   exemplification of the invention
XX
SQ   Sequence 444 AA;

  Query Match             47.1%;  Score 1273.5;  DB 6;  Length 444;
  Best Local Similarity   59.3%;  Pred. No. 7.8e-63;
  Matches  275;  Conservative   27;  Mismatches   69;  Indels   93;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFL-----TKGPSKL 76
              | | | :: |:| ||     |    |      |    :  : : ||:       ||   :
Db         11 LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: ||: | |      :|: ||:  | |  :           ||          |
Db         71 S-RDNAKNSLYLQMN------SLRAEDTAVYYCARQ----------GLD-------YWG 105

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG----------KTLSVS---------- 172
              :   :|: |     |||   :|  |:  ||             : ::||
Db        106 RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 165

Qy        173 --QLELQDSG----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                |: | |  | |    |:|       |||||||
Db        166 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 219

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 279

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 339

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 399

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||||
Db        400 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 443


RESULT 65
AAR93553
ID   AAR93553 standard; protein; 475 AA.
XX
AC   AAR93553;
XX
DT   20-AUG-1996  (first entry)
XX
DE   Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
XX
KW   Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW   65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /note= "Signal peptide"
FT   Protein         20. .475
FT                   /note= "Mature heavy chain"
XX
PN   JP08038178-A.
XX
PD   13-FEB-1996.
XX
PF   20-FEB-1995;   95JP-00030742.
XX
PR   18-FEB-1994;   94JP-00021628.
XX
PA   (TANA/) TANAKA H.
PA   (NISN ) NISSHINBO IND INC.
XX
DR   WPI; 1996-154852/16.
DR   N-PSDB; AAT18059.
XX
PT   Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT   produced by primer amplification, used in the diagnosis of hCMV
PT   infection.
XX
PS   Claim 4; Page 16-18; 22pp; Japanese.
XX
CC   The sequences given in AAR93553-54 represent the heavy and light chains
CC   respectively of a monoclonal antibody against a 65 kD antigen of human
CC   cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified
CC   using the sequences given in AAT18040-58. The monoclonal antibody may be
CC   used in the diagnosis of hCMV
XX
SQ   Sequence 475 AA;
```

```
  Query Match             47.1%;  Score 1273.5;  DB 2;  Length 475;
  Best Local Similarity   58.1%;  Pred. No. 8.4e-63;
  Matches  283;  Conservative   29;  Mismatches   98;  Indels   77;  Gaps   14;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQI 59
              :||    | |   |           | :    | |  :|: |||| |        : |     |
Db          2 KHLWPFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGDSISRSSYSWGCIRQP 61

Qy         60 KILGNQ--GSFLTKGPSKLNDRADSRRSL-WDQGN--FPLIIKNLKIEDSDTYIC-EVED 113
                 | :  |:    | :  |    || ::  |  |  | | : ::   |:  | |
Db         62 PGKGLEWIGTIYYSGSTYYNPSLKSRVTISVDASNNQFSLKLSSVTAADTAVYYCARTSP 121

Qy        114 QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------- 166
              |  ::      || :  ::  ||  :|::  |  |  |||   :|  |:  ||
Db        122 QYYDL------LTGSFPSYWGQGTLVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCL 173

Qy        167 ------KTLSVS-------------QLELQDSG-----------------TWTCTVLQN 189
                   : ::||                || ||                 |: | |  |
Db        174 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--N 231

Qy        190 QKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV 244
               |    |:|       ||||||||||     ||||||||||||||||||||||||||||
Db        232 HKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV 287

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 347

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 407

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 467

Qy        425 SLSLSPG 431
              |||||||
Db        468 SLSLSPG 474


RESULT 66
AAW11641
ID   AAW11641 standard; protein; 475 AA.
XX
AC   AAW11641;
XX
DT   13-MAY-1997  (first entry)
XX
DE   Human anti-RSV monoclonal antibody RF-2 heavy chain.
XX
KW   Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus; RSV;
KW   fusion protein; F-protein; vaccine; immunotherapy; therapy;
KW   Epstein Barr virus; immortalisation; recombinant antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Leader_peptide
FT   Region          20. .49
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          50. .56
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          57. .70
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          71. .86
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          87. .118
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          119. .134
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          135. .145
FT                   /label= FR4
FT                   /note= "framework region 4"
FT   Region          146. .475
FT                   /label= Kappa
FT                   /note= "human gamma 1 constant region"
XX
PN   WO9640252-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US010070.
XX
PR   07-JUN-1995;   95US-00488376.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Brams P,  Chamat SS,  Pan L,  Walsh EE,  Heard CJ,  Newman RA;
XX
DR   WPI; 1997-099892/09.
DR   N-PSDB; AAT61279.
XX
PT   Human monoclonal antibody specific for respiratory syncytial virus fusion
PT   protein - used for the prevention and treatment of RSV infection.
XX
PS   Example 6; Fig 11b-c; 85pp; English.
XX
CC   A polypeptide (AAW11641) comprises a leader sequence, RF-2 heavy chain
CC   variable region (see also AAW11635), and human gamma 1 constant region.
CC   RF-2 is a human monoclonal antibody (hMAb) specific for the fusion
CC   protein of respiratory syncytial virus (RSV). The polypeptide can be
CC   produced in eukaryotic host (e.g. CHO) cells transfected with vector
CC   NEOSPLA incorporating a DNA construct (AAT61279) including the RF-2 VH
CC   sequence. RF-1 and RF-2 heavy and light chains (see also AAW11638-40) are
CC   similarly produced. The transfected host cells provide a constant, stable
CC   supply of anti-RSV F-protein hMAbs for use in the treatment or prevention
CC   of RSV infection
XX
SQ   Sequence 475 AA;

  Query Match             47.1%;  Score 1273.5;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 8.4e-63;
  Matches  276;  Conservative   29;  Mismatches   99;  Indels   79;  Gaps   11;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKIL--- 62
               |: |    |     | :   | |   |: |||| |      : :  :|      | |
Db         10 LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL 69

Qy         63 ----GNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE 117
                    :  :| :    ::|:   |: ::       | : |:   |: || |      :
Db         70 ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS 124

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                 :|        |   ||   .|: |      |||   :|  |:  ||
Db        125 DSFYLF-------YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 177

Qy        167 --KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKV 193
                 : ::||               || ||                 |: | |  | ||
Db        178 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS 235

Qy        194 EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 248
               |:|       ||||||||||     ||||||||||||||||||||||||||||||
Db        236 NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 291

Qy        249 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 351
```

```
Qy        309 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 411

Qy        369 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 471

Qy        429 SPG 431
              |||
Db        472 SPG 474
```

RESULT 67
AAY97172
ID AAY97172 standard; protein; 497 AA.
XX
AC AAY97172;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 3.
XX
KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
KW ophthalmological; anti-proliferative.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .21
FT		/label= FGF-R1_signal_peptide
FT	Domain	22. .257
FT		/label= FGF-R1_extracellular_domain
FT		/note= "The Ig I segment and acid box are deleted"
FT	Domain	59. .111
FT		/label= Ig_II_segment
FT	Domain	157. .222
FT		/label= Ig_III_segment
FT	Peptide	258. .265
FT		/label= Linker
FT	Region	266. .497
FT		/label= Human_IgG1_Fc_region
FT		/note= "Contains hinge region and domains CH2 and CH3"

XX
PN WO200046380-A2.
XX
PD 10-AUG-2000.
XX
PF 07-FEB-2000; 2000WO-US003166.
XX
PR 08-FEB-1999; 99US-0119002P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Kavanaugh WM, Ballinger M;
XX
DR WPI; 2000-514961/46.
DR N-PSDB; AAA52129.
XX
PT New polypeptide comprising a fibroblast growth factor receptor
PT extracellular domain fused to a heterologous oligomerization domain for
PT treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
PS Claim 14; Page 58-59; 70pp; English.
XX
CC Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
CC receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
CC (Ig) I segment fused to a heterologous oligomerization domain that
CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
CC region, or light chain of an immunoglobulin molecule, or a peptide with a
CC leucine zipper motif. The Ig I segment is not necessary for binding of
CC acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
CC affinity for aFGF and heparin, protects the core of the molecule from
CC proteolysis, and abrogates the heparin requirement for aFGF binding. The
CC new fusion polypeptides are better FGF inhibitors than FGF-R monomer
CC proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at
CC subnanomolar concentrations and were 20-fold more potent than the FGF-R
CC monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
CC fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
CC mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung,
CC rectal, testis and cervical tumours), neovascularization (e.g. diabetic
CC retinopathy, neovascular glaucoma, wound healing and corneal scarring)
CC and hyper-proliferation of vascular smooth muscle cells (e.g.
CC postangioplasty and postatherectomy restenosis)
XX
SQ Sequence 497 AA;

Query Match 47.1%; Score 1273.5; DB 3; Length 497;
Best Local Similarity 57.5%; Pred. No. 8.8e-63;
Matches 276; Conservative 30; Mismatches 83; Indels 91; Gaps 12;

```
Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
              :|  :|||           ||:  | :|   :    | ||  : |    | | :  :
Db         45 KLHAVPAA-----------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 92

Qy         70 TKG-------PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |          ||             |:||:  |::|     : ||  :| ::     :|
Db         93 TWSIIMDSVVPS------------DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 139

Qy        123 FGLTANSDTHLLQGQSLTLTLESPP-------------GSS------PSVQCRSPRGKNI 163
               || ||    |           : | |             ||       | ||      | |
Db        140 AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT 199

Qy        164 --QGGKTLSVSQLELQDSGTWTC--------------TVLQNQKKVEFKIDIVPCP--- 203
                :  : | :  :  :|:| :||             |||:    :| :  ::  |
Db        200 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 256

Qy        204 -------APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                    ||||||||||||      |||||||||||||||||||||||||||||||||||
Db        257 EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 316

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 376

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 436

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 496
```

RESULT 68
AAY97171
ID AAY97171 standard; protein; 525 AA.
XX
AC AAY97171;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 2.
XX
KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
KW ophthalmological; anti-proliferative.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .21
FT		/label= FGF-R1_signal_peptide

```
FT   Domain          22. .285
FT                   /label= FGF-R1_extracellular_domain
FT                   /note= "Ig I segment is deleted"
FT   Domain          37. .44
FT                   /label= Acid_box_segment
FT   Domain          87. .139
FT                   /label= Ig_II_segment
FT   Peptide         286. .293
FT                   /label= Linker
FT   Region          294. .525
FT                   /label= Human_IgG1_Fc_region
FT                   /note= "Contains hinge region and domains CH2 and CH3"
FT   Domain          445. .250
FT                   /label= Ig_III_segment
XX
PN   WO200046380-A2.
XX
PD   10-AUG-2000.
XX
PF   07-FEB-2000; 2000WO-US003166.
XX
PR   08-FEB-1999;   99US-0119002P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kavanaugh WM,  Ballinger M;
XX
DR   WPI; 2000-514961/46.
DR   N-PSDB; AAA52128.
XX
PT   New polypeptide comprising a fibroblast growth factor receptor
PT   extracellular domain fused to a heterologous oligomerization domain for
PT   treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
PS   Claim 14; Page 54-55; 70pp; English.
XX
CC   Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
CC   receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
CC   (Ig) I segment fused to a heterologous oligomerization domain that
CC   comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
CC   region, or light chain of an immunoglobulin molecule, or a peptide with a
CC   leucine zipper motif. The Ig I segment is not necessary for binding of
CC   acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
CC   affinity for aFGF and heparin, protects the core of the molecule from
CC   proteolysis, and abrogates the heparin requirement for aFGF binding. The
CC   new fusion polypeptides are better FGF inhibitors than FGF-R monomer
CC   proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at
CC   subnanomolar concentrations and were 20-fold more potent than the FGF-R
CC   monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
CC   fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
CC   mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung,
CC   rectal, testis and cervical tumours), neovascularization (e.g. diabetic
CC   retinopathy, neovascular glaucoma, wound healing and corneal scarring)
CC   and hyper-proliferation of vascular smooth muscle cells (e.g.
CC   postangioplasty and postatherectomy restenosis)
XX
SQ   Sequence 525 AA;

  Query Match             47.1%;  Score 1273.5;  DB 3;  Length 525;
  Best Local Similarity   57.5%;  Pred. No. 9.4e-63;
  Matches  276;  Conservative   30;  Mismatches   83;  Indels   91;  Gaps   12;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
              :|  :|||              ||:  | :|   :    | ||  : |    | | :  :
Db         73 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120

Qy         70 TKG-------PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
              |         ||            |:||:  |::|     : ||  :| ::     :|
Db        121 TWSIIMDSVVPS------------DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 167

Qy        123 FGLTANSDTHLLQGQSLTLTLESPP------------GSS------PSVQCRSPRGKNI 163
               || ||    |         : | |                ||       | ||     | |
Db        168 AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT 227

Qy        164 --QGGKTLSVSQLELQDSGTWTC---------------TVLQNQKKVEFKIDIVPCP--- 203
                :  : | :  :  :|:| :||               |||:    :| :  ::  |
Db        228 TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL 284

Qy        204 -------APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                    ||||||||||     |||||||||||||||||||||||||||||||||||||
Db        285 EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 344

Qy        252 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 404

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 464

Qy        372 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 524


RESULT 69
AAY97170
ID   AAY97170 standard; protein; 622 AA.
XX
AC   AAY97170;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human FGF-RI Extracellular domain-Ig Fc fusion protein 1.
XX
KW   FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
KW   immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
KW   inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
KW   ophthalmological; anti-proliferative.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .21
FT                   /label= FGF-R1_signal_peptide
FT   Domain          22. .374
FT                   /label= FGF-R1_extracellular_domain
FT   Domain          55. .101
FT                   /label= Ig_I_segment
FT   Domain          126. .133
FT                   /label= Acid_box_segment
FT   Domain          176. .228
FT                   /label= Ig_II_segment
FT   Domain          275. .339
FT                   /label= Ig_III_segment
FT                   /note= "This is the IIIc variant version"
FT   Peptide         379. .390
FT                   /label= Linker
FT                   /note= "Contains trhombin cleavage site"
FT   Protein         391. .622
FT                   /label= Human_IgG1_Fc_region
FT                   /note= "Contains hinge region and domains CH2 and CH3"
XX
PN   WO200046380-A2.
XX
PD   10-AUG-2000.
XX
PF   07-FEB-2000; 2000WO-US003166.
XX
PR   08-FEB-1999;   99US-0119002P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kavanaugh WM,  Ballinger M;
XX
DR   WPI; 2000-514961/46.
```

```
DR   N-PSDB; AAA52127.
XX
PT   New polypeptide comprising a fibroblast growth factor receptor
PT   extracellular domain fused to a heterologous oligomerization domain for
PT   treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
XX
PS   Claim 14; Page 51-52; 70pp; English.
XX
CC   Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
CC   receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
CC   (Ig) I segment fused to a heterologous oligomerization domain that
CC   comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
CC   region, or light chain of an immunoglobulin molecule, or a peptide with a
CC   leucine zipper motif. The Ig I segment is not necessary for binding of
CC   acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
CC   affinity for aFGF and heparin, protects the core of the molecule from
CC   proteolysis, and abrogates the heparin requirement for aFGF binding. The
CC   new fusion polypeptides are better FGF inhibitors than FGF-R monomer
CC   proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at
CC   subnanomolar concentrations and were 20-fold more potent than the FGF-R
CC   monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
CC   fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-
CC   mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung,
CC   rectal, testis and cervical tumours), neovascularization (e.g. diabetic
CC   retinopathy, neovascular glaucoma, wound healing and corneal scarring)
CC   and hyper-proliferation of vascular smooth muscle cells (e.g.
CC   postangioplasty and postatherectomy restenosis)
XX
SQ   Sequence 622 AA;

  Query Match             47.1%;  Score 1273.5;  DB 3;  Length 622;
  Best Local Similarity   57.0%;  Pred. No. 1.1e-62;
  Matches  276;  Conservative   31;  Mismatches   86;  Indels   91;  Gaps   12;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIKILGNQGSFLTKGP 73
              :|  :|||              ||:  | :|   :    | ||  : |     | :
Db        162 KLHAVPAA------------KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKV--- 206

Qy         74 SKLNDRADSRRSLW----------DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF 123
                  | : |           |:||:  |::|     : ||  :| ::     :|
Db        207 ---------RYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQA 257

Qy        124 GLTANSDTHLLQGQSLTLTLESPP-------------GSS------PSVQCRSPRGKNI- 163
              || ||    |          : | |             ||       | ||     | |
Db        258 GLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTT 317

Qy        164 -QGGKTLSVSQLELQDSGTWTC--------------TVLQNQKK----------VEFKI 197
               :  : | :  :  :|:| :||               |||:  ::          :| :
Db        318 DKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLESRG 377

Qy        198 DIVP----CPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
               :||     |   ||||||||||     ||||||||||||||||||||||||||||||
Db        378 GLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 437

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 497

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 557

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 617

Qy        428 LSPG 431
              ||||
Db        618 LSPG 621


RESULT 70
AAB83838
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```
ID   AAB83838 standard; protein; 592 AA.
XX
AC   AAB83838;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of an Ig-5T4 fusion protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 503
FT                   /note= "Met encoded by CTG"
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   N-PSDB; AAF89733.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
XX
PS   Disclosure; Fig 6; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   represents an Ig-5T4 fusion protein
XX
SQ   Sequence 592 AA;

  Query Match             47.1%;  Score 1273;  DB 4;  Length 592;
  Best Local Similarity   59.2%;  Pred. No. 1.1e-62;
  Matches  276;  Conservative   19;  Mismatches   81;  Indels   90;  Gaps   11;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              ||    :|   || | :|| |||  |    |                 : |: |     |
Db        159 TQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKP----------GQSPTLLISYTSS 207

Qy         83 R-RSLWDQ-------GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL 134
              |   : |:         :|   |  |: ||   | |: :              ||
Db        208 RYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQD-------------YNSPPTFG 253
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Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
Db        254 GGTKLEIKRASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 311

Qy        173 ----QLELQDSG------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
Db        312 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC 365

Qy        211 DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 265
Db        366 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 425

Qy        266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
Db        426 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 485

Qy        326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
Db        486 GQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 545

Qy        386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        546 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 591
```

RESULT 71
ADE64199
ID ADE64199 standard; protein; 465 AA.
XX
AC ADE64199;
XX
DT 29-JAN-2004 (first entry)
XX
DE LL2HCF protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; LL2HCF.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT Misc-difference 153
FT   /note= "Encoded by AC in pLBC-L2HCF (SeqID1)"
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64205.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 5; 57pp; English.
XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of
CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and
CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the LL2HCF protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 465 AA;

```
  Query Match             47.1%;  Score 1272.5;  DB 7;  Length 465;
  Best Local Similarity   58.7%;  Pred. No. 9.3e-63;
  Matches  270;  Conservative   27;  Mismatches   76;  Indels   87;  Gaps   10;

Qy         32 KKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQ 89
Db         32 KPGSSVKVSCKASGYTFTSYWLHW-----VRQAPGQGLEWIGYINPRNDYTEYNQNFKDK 86

Qy         90 GNFP---------LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
Db         87 ATITADESTNTAYMELSSLRSEDTAFYFCARRD----------------ITTFYWGQGTT 130

Qy        141 LTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QL 174
Db        131 VTVSSASTKGPSVFPLAPSSKSXSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 190

Qy        175 ELQDSG------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC 216
Db        191 VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDKTHTC 244

Qy        217 -----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271
Db        245 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 304

Qy        272 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 331
Db        305 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 364

Qy        332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
Db        365 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 424

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        425 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 464
```

RESULT 72
AAB49243
ID AAB49243 standard; protein; 476 AA.
XX
AC AAB49243;
XX
DT 15-MAR-2001 (first entry)
XX
DE Chimeric 4H6 anti-DR4 antibody heavy chain protein.
XX
KW Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;
KW autoimmune.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073349-A1.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US014599.
XX
PR 28-MAY-1999; 99US-00322875.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;
XX
DR WPI; 2001-041145/05.
XX
PT Novel anti-death receptor 4 antibodies useful for treating cancer and
PT immune related disorders such as rheumatoid arthritis, sjogren's
PT syndrome, Grave's disease and diabetes mellitus.
XX
PS Claim 16; Fig 18; 126pp; English.
XX
CC The present invention relates to an anti-Death receptor 4 (DR4) antibody.
CC The antibodies of the invention are useful for inducing apoptosis in
CC mammalian cancer cells such as colon cancer cells and for treating an
CC immune-related disease in a mammal such as arthritis and autoimmune
CC disease
XX
SQ Sequence 476 AA;

Query Match 47.1%; Score 1272; DB 4; Length 476;
Best Local Similarity 60.4%; Pred. No. 1e-62;
Matches 273; Conservative 29; Mismatches 82; Indels 68; Gaps 12;

```
Qy         36 TVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNF 92
              :: :||| |      |   ||       | |   |     | :  |    || |:  |
Db         36 SLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAVGSTNYNSALMSRLSISKDNSKS 95

Qy         93 PLIIK--NLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLTLESPPG 148
               : :|  :|: :|:  | |  | : :      :| :  |  | :   ||  ::|: |
Db         96 QVFLKMNSLQTDDTAMYYCAREGEFD-----YYGSSLLS-YHSMNFWGQGTSVTVSSAKT 149

Qy        149 SSPSVQCRSPRGKNIQGG------------KTLSVS------------QLELQDSG-- 180
              : |||   :|  |:  ||             : ::||                || ||
Db        150 TGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 209

Qy        181 ---------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL 219
                            |: | |  | |    |:|       ||||||||||     |||
Db        210 SLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPEL 263

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 323

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 443

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||
Db        444 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
```

RESULT 73
AAY50151
ID AAY50151 standard; protein; 453 AA.
XX
AC AAY50151;
XX
DT 17-OCT-2003 (revised)
DT 31-JAN-2000 (first entry)
XX
DE Antibody F19 chimeric mouse/human heavy chain variable region (chF19HC).
XX
KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
KW humanisation; complementarity determining region; CDR; CDR grafting;
KW reactive stroma; fibroblast; epithelial cancer; diagnosis;
KW immune response; framework sequence; constant region; variable region;
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;
KW skin inflammmation; tumour; immunogenicity; chimeric; heavy chain.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN EP953639-A1.
XX
PD 03-NOV-1999.
XX
PF 30-APR-1998; 98EP-00107925.
XX
PR 30-APR-1998; 98EP-00107925.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
PI Rettig WJ;
XX
DR WPI; 1999-621833/54.
XX
PT New antibody protein, useful for treating cancer and for imaging presence
PT of activated stromal fibroblasts in healing wound or inflamed skin.
XX
PS Example 1; Fig 18; 143pp; English.
XX
CC This sequence represents the heavy chain variable region of a chimeric
CC mouse/human F19 antibody (chF19HC). F19 (ATCC Accession number HB 8269)
CC is a murine monoclonal antibody against fibroblast activation protein
CC alpha (FAP). FAP is a cell surface molecule of reactive stromal
CC fibroblasts, and its induction is a highly consistent molecular trait of
CC the reactive stroma of many types of epithelial cancer. Although F19 may
CC be useful in vitro, e.g., for diagnosis, its applications for in vivo use
CC in humans are problematic as it elicits a human anti-mouse response which
CC reduces the efficacy of the antibody in patients and impairs continued
CC administration. This chimeric antibody was humanised by joining entire
CC murine variable regions to human constant regions. However, humanised
CC antibodies produced by this method can still elicit an anti-mouse
CC response in humans, whereas antibodies humanised via CDR (complementarity
CC determining region) grafting are less immunogenic in humans. Humanised
CC F19 antibodies are useful for treating cancers e.g., colorectal cancers,
CC non-small cell lung cancers, breast cancers, head and neck cancers,
CC ovarian cancers, lung cancers, bladder cancers, pancreatic cancers and
CC metastatic cancers. They are also useful for the detection of activated
CC stromal fibroblasts in a healing wound, inflamed skin or a tumour in a
CC human patient. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 453 AA;

Query Match 47.1%; Score 1271.5; DB 2; Length 453;
Best Local Similarity 59.0%; Pred. No. 1e-62;
Matches 271; Conservative 31; Mismatches 84; Indels 73; Gaps 12;

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Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL 86
              | | | :|:::|  |:    ::  ||   :  | |   |       |    | :   | :|
Db         10 LVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLEWIGGINPNNGIPNYNQKFKGRATL 69

Qy         87 W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
                    : :::|  |||  | |         : : :|     : | :   ||  ::
Db         70 TVGKSSSTAYMELRSLTSEDSAVYFC-------ARRRIAYGY---DEGHAMDYWGQGTSV 119

Qy        142 TLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLE 175
              |: |     |||   :|  |:  ||             : ::||
Db        120 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC- 216
              || ||                |: | |  | |    |:|       ||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP 233

Qy        217 ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 293

Qy        273 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 353

Qy        333 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 392
                |||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 413

Qy        393 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                |||||||||||||||||||||||||||||||||||||||
Db        414 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 452
```

RESULT 74
ABG31025
ID ABG31025 standard; protein; 499 AA.
XX
AC ABG31025;
XX
DT 05-NOV-2002 (first entry)
XX
DE Synthetic mouse/human chimeric fusion protein #1.
XX
KW Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;
KW neuroprotective; gene therapy; single chain antibody; variable fragment;
KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;
KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
KW ulcerative colitis; inflammatory bowel disease; immunological effector;
KW cell mediated cytotoxicity; complement dependent cytotoxicity;
KW complement fixation; mouse; human.
XX
OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key   Location/Qualifiers
FT Region   1. .265
FT   /note= "Mouse anti-human CD20 single chain variable
FT   fragment (scFv)"
FT Domain   266. .499
FT   /note= "Human immunoglobulinG1 (IgG1) wild type hinge,
FT   fragment of crystallisation, CH2 and CH3 domains"
XX
PN WO200256910-A1.
XX
PD 25-JUL-2002.
XX
PF 17-JAN-2002; 2002WO-US001487.
XX
PR 17-JAN-2001; 2001US-00765208.
XX
PA (GENE-) GENECRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter M;
XX
DR WPI; 2002-599691/64.
DR N-PSDB; ABK89848.
XX
PT New human binding domain-immunoglobulin fusion protein useful for
PT treating a subject having or suspected of having a B-cell disorder or
PT malignant condition e.g. rheumatoid arthritis.
XX
PS Disclosure; Page 120-121; 136pp; English.
XX
CC The invention describes a binding domain-immunoglobulin fusion protein
CC that is capable of at least one immunological activity, comprising a
CC binding domain polypeptide fused to an immunoglobulin hinge region
CC polypeptide capable of specifically binding to an antigen, or an
CC immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
CC to the hinge region polypeptide or to the CH2 constant region
CC polypeptide. The fusion protein is useful for treating a subject having
CC or suspected of having a B-cell disorder or malignant condition e.g.
CC rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's
CC thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
CC erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura,
CC psoriasis, scleroderma, cancer and inflammatory bowel disease such as
CC Chron's disease and ulcerative colitis. The fusion protein retains the
CC ability to participate in well known immunological effector activities
CC including antibody dependent cell mediated cytotoxicity and/or complement
CC fixation in complement dependent cytotoxicity, despite having structures
CC that would not be expected to be capable of promoting the effector
CC activities. It can be produced in substantial quantities that are
CC typically greater than those routinely attained with single-chain
CC antibody constructs. This is the amino acid sequence of a chimeric fusion
CC protein created from the mouse anti-human CD20 single chain antibody
CC variable fragment (scFv) and the human immunoglobulin G (IgG) fragment of
CC crystallisation (Fv) tail, wild type hinge, CH2 and CH3 domains
XX
SQ Sequence 499 AA;

```
  Query Match             47.1%;  Score 1271.5;  DB 5;  Length 499;
  Best Local Similarity   56.6%;  Pred. No. 1.1e-62;
  Matches  275;  Conservative   27;  Mismatches   93;  Indels   91;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||         |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |   | :: | |  :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR----------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:                  :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                         :  :|  ||:|            | |  :||  : |  :       :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
              |:      |     ||||||||||     |||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 312

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 432

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 492

Qy        426 LSLSPG 431
              ||||||
Db        493 LSLSPG 498
```

RESULT 75
ADD25587
ID ADD25587 standard; protein; 499 AA.
XX
AC ADD25587;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #71.
XX
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;

```
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 148; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 499 AA;
```

```
  Query Match             47.1%;  Score 1271.5;  DB 7;  Length 499;
  Best Local Similarity   56.6%;  Pred. No. 1.1e-62;
  Matches  275;  Conservative   27;  Mismatches   93;  Indels   91;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||  .     |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKGGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR----------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:                  :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :       :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
                |:      |     ||||||||||     ||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 312

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 432

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 492

Qy        426 LSLSPG 431
              ||||||
Db        493 LSLSPG 498
```

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RESULT 76
ADD25454
ID   ADD25454 standard; protein; 499 AA.
XX
AC   ADD25454;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated protein #5.
XX
KW   Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
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```
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 15; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 499 AA;

  Query Match             47.1%;  Score 1271.5;  DB 7;  Length 499;
  Best Local Similarity   56.6%;  Pred. No. 1.1e-62;
  Matches  275;  Conservative   27;  Mismatches   93;  Indels   91;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||         |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL--------------- 125
              | |     | :: | |  :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---------------SPR------ 159
                 :|  :| | |  |       ||:|  : |:              :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :       :
```

```
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
               |:      |     ||||||||||     ||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 312

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 432

Qy        366 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 492

Qy        426 LSLSPG 431
              ||||||
Db        493 LSLSPG 498


RESULT 77
ABP58275
ID   ABP58275 standard; protein; 468 AA.
XX
AC   ABP58275;
XX
DT   23-OCT-2003  (revised)
DT   31-MAR-2003  (first entry)
XX
DE   Humanised 3D6 antibody heavy chain.
XX
KW   Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
KW   human; humanised antibody; antibody; Alzheimer's disease;
KW   Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .468
FT                   /label= Mature_peptide
FT                   /note= "the mature heavy chain is claimed in Claim 5"
FT   Region          20. .138
FT                   /note= "heavy chain variable region, claimed in Claim 4"
FT   Region          50. .54
FT                   /note= "CDR1"
FT   Region          69. .85
FT                   /note= "CDR2"
FT   Region          118. .127
FT                   /note= "CDR3"
XX
PN   WO200288306-A2.
XX
PD   07-NOV-2002.
XX
PF   26-APR-2002; 2002WO-US011853.
XX
PR   30-APR-2001; 2001US-0287539P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Tsurushita N,  Vasquez M;
XX
DR   WPI; 2003-183835/18.
DR   N-PSDB; ABZ24633, ABZ24635.
XX
PT   New humanized forms of mouse 3D6 antibodies, useful for treating Down's
```

```
PT   syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
PT   amyloid angiopathy, or for inhibiting formation of or reducing Abeta
PT   plaque in the brain.
XX
PS   Disclosure; Page 13-14; 54pp; English.
XX
CC   The present sequence is that of a preferred heavy chain of a humanised
CC   antibody of the present invention. In the variable region of this
CC   sequence, the complementarity determining regions (CDRs) originate from
CC   murine monoclonal antibody 3D6 and the framework region from human
CC   germline VH segment DP-45 and J segment JH4. Novel humanised antibodies
CC   of the invention have CDRs from 3D6 and human framework sequences. These
CC   humanised antibodies have binding affinities (affinity and epitope
CC   location) approximately the same as those of the mouse 3D6 antibody. The
CC   invention includes antibodies, single chain antibodies, and their
CC   fragments, as well as nucleotide sequences, vectors, transformed host
CC   cells, and methods of using the humanised antibody to treat, prevent,
CC   alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC   associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC   (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC   reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 468 AA;

  Query Match             47.0%;  Score 1271;  DB 6;  Length 468;
  Best Local Similarity   57.0%;  Pred. No. 1.1e-62;
  Matches  284;  Conservative   31;  Mismatches   85;  Indels   98;  Gaps   15;

Qy          1 MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS------------ 44
              ||.|:    |:|||   |  :    : |  |   : | :: |:|  |
Db          1 MNFGLSLIFLVLVLKGVQCEVQLVESGGGLV---QPGGSLRLSCAGSGFTFSNYGMSWVR 57

Qy         45 QKKSIQFHWKNSNQIKILGNQGSFL--TKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIE 102
              |       |  |  |:  | :  :    ||   :: | ::: ||: | |      :|: |
Db         58 QAPGKGLEWVAS--IRSGGGRTYYSDNVKGRFTIS-RENAKNSLYLQMN------SLRAE 108

Qy        103 DSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKN 162
              |:  | |   |             : :||     ||   :|: |     |||   :|  |:
Db        109 DTAVYYCVRYDH----------YSGSSD---YWGQGTLVTVSSASTKGPSVFPLAPSSKS 155

Qy        163 IQGG-------------KTLSVS-------------QLELQDSG---------------- 180
              ||              : ::||                || ||
Db        156 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG 215

Qy        181 --TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPK 233
                |: | |  | |    |:|        ||||||||||     ||||||||||||||||
Db        216 TQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK 269

Qy        234 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 329

Qy        294 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 389

Qy        354 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 449

Qy        414 HEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||
Db        450 HEALHNHYTQKSLSLSPG 467


RESULT 78
AAR93166
ID   AAR93166 standard; protein; 472 AA.
XX
AC   AAR93166;
XX
DT   30-OCT-1996  (first entry)
XX
DE   Anti-rhesus D recombinant antibody D7C2 heavy chain.
XX
KW   Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
KW   rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;
KW   variable region; insect host cell; baculovirus; recombinant production.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= signal_peptide
FT                   /note= "mouse VH signal peptide sequence encoded by
FT                   synthetic linker"
FT   Protein         20. .472
FT                   /label= heavy_chain
FT                   /note= "human gamma 1 chain constant region and the
FT                   variable region from anti-rhesus D antibody D7C2"
XX
PN   FR2724182-A1.
XX
PD   08-MAR-1996.
XX
PF   02-SEP-1994;   94FR-00010566.
XX
PR   02-SEP-1994;   94FR-00010566.
XX
PA   (INSP ) INST PASTEUR.
PA   (PROT-) PROTEINE PERFORMANCE.
XX
PI   Edelman L,  Margaritte C,  Kaczorek M,  Chaabihi H;
XX
DR   WPI; 1996-162018/17.
DR   N-PSDB; AAT26889.
XX
PT   Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-
PT   transformed insect cells and useful for preventing haemolysis in new-born
PT   babies.
XX
PS   Example 2; Page 35-37; 46pp; French.
XX
CC   The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD
CC   polypeptide on the membrane of rhesus positive red blood cells. The
CC   antibody agglutinates rhesus positive cells but not rhesus negative cells
CC   and is useful diagnostically and also for preventing haemolysis in new-
CC   born rhesus positive babies. Recombinant IgM-D7C2 can be produced by
CC   insect cells which have been transformed by a baculoviral vector
CC   comprising a D7C2 expression cassette. The present sequence is that of a
CC   recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal
CC   peptide
XX
SQ   Sequence 472 AA;

  Query Match             47.0%;  Score 1271;  DB 2;  Length 472;
  Best Local Similarity   59.5%;  Pred. No. 1.2e-62;
  Matches  270;  Conservative   25;  Mismatches   91;  Indels   68;  Gaps    9;

Qy         32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQ--GSFLTKGPSKLNDRADSRRSL--- 86
              |  :|: ||||        ::|    |    | :  |     | :  |    || ::
Db         32 KPSETLSLTCTVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVD 91

Qy         87 WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
                 :  | | : ::   |:  | |    :        :    : |      ||  |:|: |
Db         92 TSKNQFSLKLNSVTAADTAVYYCARAPE--------YKWKYHGDWFDPWGQGTTVTVSSA 143

Qy        147 PGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG 180
                 |||   :|  |:  ||              : ::||                || ||
Db        144 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 203

Qy        181 -----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----P 217
                              |: | |  | |    |:|       ||||||||||     |
Db        204 LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAP 257
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Qy        218 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 317

Qy        278 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 337
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        318 EEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 377

Qy        338 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 437

Qy        398 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||
Db        438 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471
```

RESULT 79
AAW01822
ID AAW01822 standard; protein; 476 AA.
XX
AC AAW01822;
XX
DT 17-OCT-2003 (revised)
DT 25-MAY-1997 (first entry)
XX
DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopaenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma;
KW transfectoma.
XX
OS Macaca; cynomolgus.
OS Homo sapiens.
OS Chimeric.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US010053.
XX
PR 07-JUN-1995; 95US-00487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR WPI; 1997-108638/10.
DR N-PSDB; AAT62513.
XX
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen - useful
PT for treating auto:immune disease or graft-versus-host disease.
XX
PS Claim 14; Fig 10B; 81pp; English.
XX
CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human B7.1
CC antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable
CC genes (see also AAT62512 and AAT62513) are inserted into an expression
CC vector (pref. NEOSPLA) which contains human light and heavy chain
CC constant region genes to allow prodn. of the primatised antibody in e.g.
CC CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been
CC produced (see also AAW01817-20). The primatised antibodies inhibit the
CC B7:CD28 pathway, making them useful immunosuppressants for the treatment
CC of autoimmune disorders and graft-versus-host disease. (Updated on 17-OCT
CC -2003 to standardise OS field)
XX
SQ Sequence 476 AA;

Query Match 47.0%; Score 1271; DB 2; Length 476;
Best Local Similarity 59.8%; Pred. No. 1.2e-62;
Matches 274; Conservative 29; Mismatches 87; Indels 68; Gaps 11;

```
Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |         : |      | |   |||  : | :  |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
              :     :  | | : ::   |:  | | | |:   |  :|:     ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------QLEL 176
              : |     |||   :|  |:  ||             : ::||            |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                 |: | |  | |    |:|       ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
```

RESULT 80
AAW63765
ID AAW63765 standard; protein; 476 AA.
XX
AC AAW63765;
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatized 16C10 heavy chain protein.
XX
KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation.
XX
OS Macaca fascicularis.
XX
PN WO9819706-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97WO-US019906.
XX
PR 08-NOV-1996; 96US-00746361.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Hanna N, Brams P;
XX
DR WPI; 1998-286601/25.
DR N-PSDB; AAV35489.
XX
PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants for

```
PT   treating diseases that involve interactions between T and B cells, e.g.
PT   graft rejection or tumours.
XX
PS   Example 7; Fig 5b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 16C10 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the MAb
CC   can be conjugated to a drug or toxin. MAb's, or their fragments, can also
CC   be used as imaging agents and as vaccines or immunogens to develop anti-
CC   idiotype reagents. MAb's are optionally combined with other proteins or
CC   small molecule immunosuppressants. Blocking B7/CD28 interactions induces
CC   long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and antigen-
CC   specific immunoglobulin G (IgG) responses
XX
SQ   Sequence 476 AA;

  Query Match             47.0%;  Score 1271;  DB 2;  Length 476;
  Best Local Similarity   59.8%;  Pred. No. 1.2e-62;
  Matches  274;  Conservative   29;  Mismatches   87;  Indels   68;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |         .: |      | |   |||  : | :  |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
              :    :  | | : ::   |:  | | | |:   |  :|:     ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLEL 176
              : |     |||   :|  |:  ||             : ::||             |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                 |: | |  | |    |:|       ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257

Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475


RESULT 81
AAU11646
ID   AAU11646 standard; protein; 476 AA.
XX
AC   AAU11646;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Protein sequence of primatised form of the heavy chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection; interleukin-2;
KW   IL-2; mutant; mutein.
XX
OS   Homo sapiens.
OS   Macaca sp.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US016364.
XX
PR   22-MAY-2000; 2000US-00576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Hanna N,  Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17247.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen CD80
PT   and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating
PT   cancer, graft-vs-host disease and autoimmune disease such as allergy.
XX
PS   Example 8; Fig 5b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody which
CC   specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for
CC   inducing the apoptosis of B7+ cells. The invention is useful for treating
CC   diseases such as B cell cancer, lymphoma, a cancer where B cells promote
CC   the growth and/or metastasis of tumours, B cell lymphoma, B cell
CC   leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia
CC   purpura, systemic lupus, erythematosus, type 1 diabetes mellitus,
CC   rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile
CC   disease, allergy, multiple sclerosis or graft-vs-host disease. The
CC   antibody is useful for immunosuppression in a human or animal and for
CC   treating or preventing resistance to or rejection of transplanted organ
CC   or tissue for treating proliferative and hyperproliferative diseases, for
CC   treating reversible obstructive airways disease, intestinal inflammations
CC   and allergies e.g. Crohn's disease and ulcerative colitis, food-related
CC   allergies e.g. migraine, rhinitis and eczema, and other types of
CC   allergies. The present protein sequence represents the heavy chain of
CC   16C10, a primatised antibody used in the invention to induce apoptosis
CC   and inhibit production of interleukin-2 (IL-2)
XX
SQ   Sequence 476 AA;

  Query Match             47.0%;  Score 1271;  DB 5;  Length 476;
  Best Local Similarity   59.8%;  Pred. No. 1.2e-62;
  Matches  274;  Conservative   29;  Mismatches   87;  Indels   68;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85
              | |  :|: |||  |         .: |      | |   |||  : | :  |    |: :
Db         30 LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT 89

Qy         86 L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
              :    :  | | : ::   |:  | | | |:   |  :|:     ::   : |  : :|
Db         90 ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT 143

Qy        143 LESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLEL 176
              : |     |||   :|  |:  ||             : ::||             |
Db        144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203

Qy        177 QDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-- 216
              | ||                 |: | |  | |    |:|       ||||||||||
Db        204 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP 257
```

```
Qy        217 ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377

Qy        334 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437

Qy        394 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||
Db        438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
```

RESULT 82
ADD25787
ID ADD25787 standard; protein; 504 AA.
XX
AC ADD25787;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #160.
XX
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
PF 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENECRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
DR WPI; 2003-801317/75.
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 348; 157pp; English.
XX
CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 504 AA;

Query Match 47.0%; Score 1271; DB 7; Length 504;
Best Local Similarity 55.0%; Pred. No. 1.2e-62;
Matches 282; Conservative 29; Mismatches 92; Indels 110; Gaps 13;

```
Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---KNSN 57
              |:|||  :              ||    :    || | ::| |||      :|   |
Db         19 MSRGVDIQ------------MTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDG 65

Qy         58 QIKILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKE 116
               :|:|    : |   |:|:    || |    | :: | | ||: ||  || |:
Db         66 TVKLL----IYYT---SRLHSGVPSRFSGSGSGTDYSLTIANLQPEDIATYFCQ------ 112

Qy        117 EVQLLVFGLTANSDTHLLQGQSL------------------TLTLESP----PGSSPSV 153
               |     |   | |:  : |                    |    |    ||:| |
Db        113 --QGNTLPWTFGGGTKLVTKRELGGGGSGGGGSGGGGSIDEVQLQQSGPELVKPGASMSC 170

Qy        154 QC------------RSPRGKNIQ------------------GGKTLSVSQ-------- 173
              :            :  |||::                  |  ||:| :
Db        171 KASGYSFTGYIVNWLKQSHGKNLEWIGLINPYKGLTTYNQKFKGKATLTVDKSSSTAYME 230

Qy        174 ---LELQDSGTWTCTVLQNQKKVEFKID-------IVPCPAPEPKSCDKTHTC-----PE 218
                 |  :||  : |          ::  |       :       ||||||||||     ||
Db        231 LLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTVSSDQEPKSCDKTHTCPPCPAPE 290

Qy        219 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 350

Qy        279 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 410

Qy        339 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 470

Qy        399 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||
Db        471 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 503
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RESULT 83

```
ABP58289
ID   ABP58289 standard; protein; 472 AA.
XX
AC   ABP58289;
XX
DT   23-OCT-2003  (revised)
DT   31-MAR-2003  (first entry)
XX
DE   Humanised 10D5 antibody heavy chain.
XX
KW   Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW   mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW   Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Peptide         20. .472
FT                   /label= Mature_protein
FT                   /note= "the mature light chain is claimed in Claim 5"
FT   Region          20. .142
FT                   /note= "light chain variable region, claimed in Claim 4"
FT   Region          50. .56
FT                   /note= "CDR1"
FT   Region          71. .86
FT                   /note= "CDR2"
FT   Region          119. .131
FT                   /note= "CDR3"
XX
PN   WO200288307-A2.
XX
PD   07-NOV-2002.
XX
PF   26-APR-2002; 2002WO-US011854.
XX
PR   30-APR-2001; 2001US-0287653P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Hinton PR,  Vasquez M;
XX
DR   WPI; 2003-183836/18.
DR   N-PSDB; ABZ24639, ABZ24641.
XX
PT   New humanized 10D5 antibody, useful for the manufacture of a medicament
PT   for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT   disease or cerebral amyloid angiopathy.
XX
PS   Disclosure; Page 13-15; 52pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain of a
CC   humanised antibody of the present invention. In the variable portion, the
CC   complementarity determining regions (CDRs) originate from murine
CC   monoclonal antibody 10D5 and the framework region originates from human
CC   germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC   of the invention have CDRs from 10D5 and human framework sequences. These
CC   humanised antibodies have binding affinities (affinity and epitope
CC   location) approximately the same as those of the mouse 10D5 antibody. The
CC   invention includes antibodies, single chain antibodies, and their
CC   fragments, as well as nucleotide sequences, vectors, transformed host
CC   cells, and methods of using the humanised antibody to treat, prevent,
CC   alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC   associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC   (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC   reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 472 AA;
```

```
  Query Match           47.0%;  Score 1270.5;  DB 6;  Length 472;
  Best Local Similarity  58.2%;  Pred. No. 1.2e-62;
  Matches  279;  Conservative   27;  Mismatches  100;  Indels   73;  Gaps   11;

Qy         10 LLLVLQLALLPAAT-QGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKILGN 64
              |||::   :|   | : :  || |  :|: |||| |        :   |       | |
Db          9 LLLIVPAYVLSQVTLKESGPVLVKPTETLTLTCTFSGFSLSTSGMGVSWIRQPPGKALEW 68

Qy         65 QGSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL 121
                     : |    || ::     :    | : |:   |: || |    ::    :|
Db         69 LAHIYWDDDKRYNPSLKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCV---RRPITPVL 125

Qy        122 VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KT 168
              |       |     ||   :|: |      |||   :|  |:  ||            :
Db        126 V-------DAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP 178

Qy        169 LSVS-------------QLELQDSG-----------------TWTCTVLQNQKKVEFKI 197
              ::||               || ||                 |: | |  | |    |:
Db        179 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKV 236

Qy        198 DIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 252
              |      ||||||||||||     ||||||||||||||||||||||||||||||||||||
Db        237 D----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 292

Qy        253 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 352

Qy        313 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 412

Qy        373 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471
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RESULT 84
AAB81987
ID   AAB81987 standard; protein; 582 AA.
XX
AC   AAB81987;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Claim 41; Page 168-172; 183pp; Japanese.
```

```
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 582 AA;

  Query Match             47.0%;  Score 1270;  DB 4;  Length 582;
  Best Local Similarity   61.0%;  Pred. No. 1.6e-62;
  Matches  271;  Conservative   26;  Mismatches   57;  Indels   90;  Gaps   12;

Qy         63 GNQGSFLT---KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ 119
              |  |:: :   ||   :: | :|: :|:      | :::|: |||  | |       |:
Db         54 GGSGTYYSDSVKGRFTIS-RDNSKNTLY------LQMRSLRAEDSAVYFC------TRVK 100

Qy        120 LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------- 166
              |  :   :        ||   ||: |     |||   :|  |:  ||
Db        101 LGTYYFDS-------WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 153

Qy        167 KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKKVEF 195
              : ::||                 || ||                 |: | |  | |
Db        154 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNT 211

Qy        196 KIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 250
              |:|       ||||||||||     ||||||||||||||||||||||||||||||||
Db        212 KVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 267

Qy        251 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 327

Qy        311 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 387

Qy        371 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 447

Qy        431 G------------LQLDETCAEAQ 442
              |           |||:    : |
Db        448 GKAPTSSSTKKTQLQLEHLLLDLQ 471


RESULT 85
AAU87089
ID   AAU87089 standard; protein; 619 AA.
XX
AC   AAU87089;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Siglec-BMS-L3a-hIg fusion protein (Siglec-BMS-L3a-hIg).
XX
KW   Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
KW   immune system disease; leukaemia; allergy; inflammatory disease;
KW   tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
KW   psoriasis; rheumatoid arthritis; conjunctivitis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200208257-A2.
XX
PD   31-JAN-2002.
XX
PF   20-JUL-2001; 2001WO-US023082.
XX
PR   21-JUL-2000; 2000US-0220139P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Longphre M,  Chang H,  Whitney G;
XX
DR   WPI; 2002-241565/29.
DR   N-PSDB; ABK43375.
XX
PT   Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
PT   molecules useful for treating immune system diseases such as asthma,
PT   leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX
PS   Example 11; Fig 23; 209pp; English.
XX
CC   The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
CC   related lectin) protein (I). Pharmaceutical compositions comprising (I)
CC   are useful for treating immune system diseases such as asthma, leukaemia
CC   or other allergic or inflammatory diseases. Extracellular domains of (I)
CC   represent potential markers for screening, diagnosis, prognosis, follow-
CC   up assays, and imaging methods. (I) is useful as a target for drugs which
CC   inhibit inflammation, tissue damage and remodeling in asthma, and
CC   inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
CC   disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
CC   also useful for monitoring the course of disease or disorders, and for
CC   identifying agents that bind with and/or modulate the biological activity
CC   of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
CC   useful in diagnosis and/or prognosis methods, and to detect the presence
CC   and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
CC   proteins in a biological sample. (II) are useful as nucleic acid probes
CC   are useful for screening genomic library to isolate a genomic clone of
CC   SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
CC   diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
CC   The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
CC   expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
CC   AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
CC   invention
XX
SQ   Sequence 619 AA;

  Query Match             47.0%;  Score 1270;  DB 5;  Length 619;
  Best Local Similarity   57.8%;  Pred. No. 1.7e-62;
  Matches  273;  Conservative   27;  Mismatches   90;  Indels   82;  Gaps   11;

Qy          8 RHLLLVLQLALLPA---ATQGNKVVL-GKKGDTVELTCTASQKKSIQFHWKNSNQIKILG 63
              | |:: :     ||     |||   |  :||  : | | |  :       |
Db        181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSW---------- 230

Qy         64 NQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQ--------- 114
                        | :|  |      |       | :  :|  ||  | |  |::
Db        231 ----------VLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALD 279

Qy        115 ------KEEVQLLVF--------GLTANSDTHLLQGQSLTL---TLESPPGSSPSVQCRS 157
                    | ::::|          |   :   :|:|||| |   |  |||
Db        280 LSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPA--------- 330

Qy        158 PRGKNIQGGKTLSVSQ-----------LELQDSGTWTCTVLQ--NQKKVEFKIDIVPCPA 204
               |    | |: || ||           ::::  | :||        : |   : :
Db        331 -RLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV---HD 386

Qy        205 PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 259
              ||||||||||||     ||  | ||||||||||||||||||||||||||||||||||||||
Db        387 PEPKSCDKTHTCPPCPAPEFEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 446

Qy        260 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 506

Qy        320 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 566

Qy        380 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 618
```

```
RESULT 86
ABB99224
ID   ABB99224 standard; protein; 448 AA.
XX
AC   ABB99224;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Chimeric CD45RO/RB binding molecule heavy chain.
XX
KW   Human; CD45; CD45RO; CD45RB; binding molecule; CDR1; CDR2; CDR3;
KW   immunosuppressive; antipsoriatic; antiinflammatory; antiallergic;
KW   CD45-Antagonist; autoimmune disease; transplant rejection; psoriasis;
KW   inflammatory bowel disease; allergy; heavy chain.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Region          31. .35
FT                   /label= CDR1
FT   Region          50. .66
FT                   /label= CDR2
FT   Region          99. .107
FT                   /label= CDR3
XX
PN   WO200272832-A2.
XX
PD   19-SEP-2002.
XX
PF   11-FEB-2002; 2002WO-EP001420.
XX
PR   12-FEB-2001; 2001GB-00003389.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Aversa G,  Kolbinger F,  Carballido Herrera JM,  Aszodi A;
PI   Saldanha JW,  Hall BM;
XX
DR   WPI; 2002-723357/78.
XX
PT   New binding molecule having at least one antigen binding site, useful as
PT   a pharmaceutical in the treatment of autoimmune diseases, transplant
PT   rejection, psoriasis, inflammatory bowel disease and allergies.
XX
PS   Claim 5; Page 31; 67pp; English.
XX
CC   The invention relates to a novel binding molecule comprising at least one
CC   antigen binding site comprising in sequence the hypervariable regions
CC   CDR1, CDR2 and CDR3. The molecule of the invention has immunosuppressive,
CC   antipsoriatic, antiinflammatory, and antiallergic activity. The molecule
CC   of the invention is a CD45-Antagonist. The binding molecule or humanised
CC   antibody is useful as a pharmaceutical in the treatment of autoimmune
CC   diseases, transplant rejection, psoriasis, inflammatory bowel disease and
CC   allergies. The binding molecule has a binding specificity for both CD45RO
CC   and CD45RB in medicine, where the binding molecule is a chimeric, a
CC   humanised or a fully human monoclonal antibody. The sequence represents
CC   the heavy chain of the CD45RO/RB binding molecule
XX
SQ   Sequence 448 AA;

  Query Match             47.0%;  Score 1269.5;  DB 5;  Length 448;
  Best Local Similarity   59.3%;  Pred. No. 1.3e-62;
  Matches  275;  Conservative   27;  Mismatches   73;  Indels   89;  Gaps   13;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HW---KNSNQIKILG-----NQGSFLTKGPSKLNDR 79
              | | | :|:::| ||      :  ||   :   :: :|     | |       :| |::
Db         11 LVKPGASVKMSCKASGYTFTNYIIHWVKQEPGQGLEWIGYFNPYNHG-------TKYNEK 63

Qy         80 ADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                 | :|         : : :|  |||  | |             |  |  ||    |

Db         64 FKGRATLTADKSSNTAYMDLSSLTSEDSAIYYCARS----------GPYAWFDT---WG 109

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS---------- 172
             |  |:|: |      |||   :|  |:  ||             : ::||
Db        110 QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 169

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |    |:|       |||||||
Db        170 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK 223

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 283

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 343

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              |||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||
Db        344 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 403

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        404 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 447


RESULT 87
AAY94408
ID   AAY94408 standard; protein; 744 AA.
XX
AC   AAY94408;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Human VCAM-1/IgGI-Fc fusion protein.
XX
KW   Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
KW   neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;
KW   dementia; epilepsy; schizophrenia; peripheral nerve injury;
KW   diabetic neuropathy; fusion protein.
XX
OS   Homo sapiens.
XX
PN   WO200032633-A1.
XX
PD   08-JUN-2000.
XX
PF   02-DEC-1999;   99WO-US028878.
XX
PR   02-DEC-1998;   98US-00203462.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Hoekstra DM,  Loughney K,  Stauton DE,  Vazeux R;
XX
DR   WPI; 2000-422952/36.
DR   N-PSDB; AAA30442.
XX
PT   Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful
PT   for diagnosing, preventing and treating diseases associated with ACAM
PT   expression and activity, e.g. epilepsy and schizophrenia.
XX
PS   Example 5; Page 174-176; 187pp; English.
XX
CC   The present sequence is a fusion protein comprising part of human VCAM-1
CC   and the Fc region of human IgGI. The sequence encoding this protein was
CC   generated by integrating the VCAM-1 coding region into a plasmid
CC   designated pDEF24/IgGI, which encodes the hinge and constant CH2-CH3
CC   domains of human IgGI. The sequence was then ligated to the expression
CC   vector pDEF24 and transformed into DH5a competent cells. The fusion
CC   protein was used as a control in adhesion experiments involving
CC   ACAM#4/IgG-Fc and ACAM#6/IgG4-Fc fusion proteins. ACAM#4 and ACAM#6 are
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CC   human foetal brain cDNA clones containing alternatively spliced full-
CC   length variants of a novel adhesion molecule designated ACAM. ACAM
CC   nucleic acids and polypeptides may be used in the prevention, treatment
CC   and diagnosis of diseases associated with inappropriate ACAM expression
CC   and activity such as dementia, epilepsy, schizophrenia, peripheral nerve
CC   injuries and diabetic neuropathies. They may be used to rectify mutations
CC   or deletions in a patient's genome that affect the activity of ACAM or to
CC   supplement insufficient ACAM production in a patient. Conversely,
CC   antisense nucleic acid molecules may be administered to down-regulate
CC   ACAM expression. The nucleotide sequence may also be used as a DNA probe
CC   in diagnostic assays (e.g. PCR) to detect and quantitate the presence of
CC   similar nucleic acid sequences in samples, and hence determine which
CC   patients may be in need of restorative therapy. ACAM polypeptides may be
CC   used as antigens in the production of antibodies against ACAM and in
CC   assays to identify modulators (agonists and antagonists) of ACAM
CC   expression and activity
XX
SQ   Sequence 744 AA;

  Query Match             47.0%;  Score 1269.5;  DB 3;  Length 744;
  Best Local Similarity   59.1%;  Pred. No. 2.3e-62;
  Matches  264;  Conservative   38;  Mismatches   65;  Indels   80;  Gaps   11;

Qy         34 GDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              ||:| |||:    :|  | |:               |:  | |: :  |  :     |
Db        328 GDSVMLTCSVMGCESPSFSWR--------------TQIDSPLSGKVRSEGT-----NST 367

Qy         94 LIIKNLKIEDSDTYICEV----EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
              | :  :  |:  :|:| |    :  :: :|: ::    : :  :  |            ||
Db        368 LTLSPVSFENEHSYLCTVTCGHKKLEKGIQVELYSFPRDPEIEMSGG--------LVNGS 419

Qy        150 SPSVQCRSP-------------RGKNIQGG---------KTLSVSQLE------LQDSG- 180
              | :| |: |             :|: |             |:|    ||      ::|:|
Db        420 SVTVSCKVPSVYPLDRLEIELLKGETILENIEFLEDTDMKSLENKSLEMTFIPTIEDTGK 479

Qy        181 TWTCTVLQNQKKVEFK-----------IDIVPCPAPEPKSCDKTHTC-----PELLGGPS 224
                 |    :   :||:           ::: |    :||||||||||     ||||||||
Db        480 ALVCQAKLHIDDMEFEPKQRQSTQTLYVNVAPV---DPKSCDKTHTCPPCPAPELLGGPS 536

Qy        225 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 596

Qy        285 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 656

Qy        345 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 716

Qy        405 GNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||
Db        717 GNVFSCSVMHEALHNHYTQKSLSLSPG 743


RESULT 88
ABB82300
ID   ABB82300 standard; protein; 634 AA.
XX
AC   ABB82300;
XX
DT   22-JAN-2003  (first entry)
XX
DE   CD19:zeta chimeric immunoreceptor.
XX
KW   CD19; chimeric; receptor; CD19R:zeta; cytostatic; immunosuppressive; CD4;
KW   antiarthritic; antiinflammatory; gene therapy; CD8; immunotherapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         23. .634
FT                   /note= "specifically claimed fragment"
XX
PN   WO200277029-A2.
XX
PD   03-OCT-2002.
XX
PF   07-NOV-2001; 2001WO-US042997.
XX
PR   07-NOV-2000; 2000US-0246117P.
XX
PA   (CITY ) CITY OF HOPE.
XX
PI   Jensen MC,  Forman S,  Raubitschek A;
XX
DR   WPI; 2003-018888/01.
DR   N-PSDB; ABV73341.
XX
PT   Genetically engineered CD19-specific immune cells, useful for cellular
PT   immunotherapy of CD19 malignancies and for abrogating any untoward B cell
PT   function in autoimmune disorders such as lupus or rheumatoid arthritis.
XX
PS   Claim 12; Fig 1A-C; 81pp; English.
XX
CC   The invention relates to genetically engineered CD19-specific immune
CC   cells which express, and bear on the cell surface membrane, a CD19-
CC   specific chimeric receptor. The CD19-specific chimeric T cell receptor
CC   consists of: (a) an intracellular signaling domain selected from zeta,
CC   eta, delta, gamma or epsilon chain pf CD3, MB1 chain, B29, FcgammaRIII
CC   and FcepsilonRI, for an effector function of the immune cell; (b) at
CC   least 1 transmembrane domain and (c) at least 1 extracellular domain
CC   comprising a CD19-specific receptor. The compositions and methods of the
CC   present invention are useful for cellular immunotherapy of CD19
CC   malignancies and for abrogating any untoward B cell function in
CC   autoimmune disorders such as lupus or rheumatoid arthritis. The present
CC   sequence represents a CD19:zeta chimeric immunoreceptor amino acid
CC   sequence. This chimeric receptor was constructed by PCR splice overlap
CC   extension and consists of human GM-CSF receptor alpha chain leader
CC   peptide, FMC63 Vh, Gly-Ser linker, FMC63 Vl, human IgG1 FC, human CD4
CC   transmembrane domain and human cytoplasmic zeta chain
XX
SQ   Sequence 634 AA;

  Query Match             46.9%;  Score 1268;  DB 6;  Length 634;
  Best Local Similarity   56.2%;  Pred. No. 2.3e-62;
  Matches  287;  Conservative   28;  Mismatches   94;  Indels  102;  Gaps   16;

Qy         10 LLLVLQLAL--LP----------AATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---K 54
              ||||  | |  ||           ||    :    || | ::| |||  |   :|   |
Db          2 LLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK 61

Qy         55 NSNQIKILGNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVED 113
                 :|:|    | |  | ||: :             :: | | ||: ||  || |:  :
Db         62 PDGTVKLLIYHTSRLHSGVPSRFSGSGSGT-------DYSLTISNLEQEDIATYFCQQGN 114

Qy        114 QKE-----EVQLLVFGLTANSDTHLLQGQSLT----LTLESPPG-----SSPSVQC---- 155
                  :| : | |: |       |:  |        || ||       | || |
Db        115 TLPYTFGGGTKLEITGSTSGSGKP-GSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSG 173

Qy        156 ----------RSPRGKNIQ------GGKT----------------------LSVSQLE 175
                       | |  | ::      | :|                      | :: |:
Db        174 VSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQ 233

Qy        176 LQDSGTWTCTVLQNQKKV----EFKIDI------VPCPAPEPKSCDKTHTC-----PELL 220
                |:  : |       |       : :|       |   : |||| ||||||     ||||
Db        234 TDDTAIYYCA-----KHYYYGGSYAMDYWGQGTSVTVSSVEPKSSDKTHTCPPCPAPELL 288

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 348

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        349 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 408

Qy        341 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 468

Qy        401 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||
Db        469 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 499


RESULT 89
ABR39465
ID   ABR39465 standard; protein; 442 AA.
XX
AC   ABR39465;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Humanised anti-Abeta antibody 266 heavy chain.
XX
KW   Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW   immunostimulant.
XX
OS   Homo sapiens.
XX
PN   WO2003016467-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US021324.
XX
PR   17-AUG-2001; 2001US-0313576P.
PR   28-MAY-2002; 2002US-0383851P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bales KR,  Paul SM;
XX
DR   WPI; 2003-289975/28.
XX
PT   Treating or reducing the progression of diseases associated with amyloid-
PT   beta peptide, e.g. Alzheimer's disease, vascular dementia or mild
PT   cognitive impairment, comprises administering an anti-amyloid-beta
PT   peptide antibody.
XX
PS   Disclosure; Page 20-22; 84pp; English.
XX
CC   The invention relates to treating cognitive symptoms or reducing disease
CC   progression in a subject having a condition or disease associated with
CC   amyloid-beta peptide (Abeta). The method involves administering an amount
CC   of an anti-Abeta antibody that has greater affinity for soluble Abeta
CC   than 10^-^9 M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42
CC   higher than 10^-^9 M, or that has greater affinity for soluble Abeta than
CC   antibody 266 has. The method or the anti-Abeta antibody is useful in
CC   preparing a medicament for treating cognitive symptoms or reducing
CC   disease progression in a subject having a condition or disease associated
CC   with Abeta. The condition or disease is Alzheimer's disease, Down's
CC   syndrome, cerebral amyloid angiopathy, vascular dementia, or mild
CC   cognitive impairment. The present sequence represents a humanised anti-
CC   Abeta antibody 266 heavy chain
XX
SQ   Sequence 442 AA;

  Query Match             46.9%;  Score 1267.5;  DB 6;  Length 442;
  Best Local Similarity   59.1%;  Pred. No. 1.7e-62;
  Matches  274;  Conservative   26;  Mismatches   69;  Indels   95;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNS---------NQIKILGNQGSF--LTKGPSKL 76
              | : | :: |:| ||          |              ||  :||   :    ||   :
Db         11 LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: :|: | |      :|: ||:  | |               |: |     |
Db         71 S-RDNAKNTLYLQMN------SLRAEDTAVYYC----------------ASGD---YWG 103

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS---------- 172
              |   :|: |     |||   :|  |:  ||             : ::||
Db        104 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 163

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                  |: | |  | |    |:|       |||||||
Db        164 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 217

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 277

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 337

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 397

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||
Db        398 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 90
ABU08311
ID   ABU08311 standard; protein; 442 AA.
XX
AC   ABU08311;
XX
DT   22-MAY-2003  (first entry)
XX
DE   Humanised 266 antibody heavy chain.
XX
KW   Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody;
KW   cognitive impairment; Alzheimer's disease; Down's syndrome;
KW   cerebral amyloid angiopathy; vascular dementia; nootropic; neurotropic;
KW   mild cognitive impairment; antibody 266; heavy chain; humanised; mutant;
KW   mutein.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO2003015691-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US021323.
XX
PR   17-AUG-2001; 2001US-0313222P.
PR   28-MAY-2002; 2002US-0383846P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bales KR,  Dodart JF,  Paul SM;
XX
DR   WPI; 2003-268234/26.
XX
PT   Effecting rapid improvement of cognition in a subject having Alzheimer's
PT   disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitive
PT   impairment, comprises administering anti-A beta antibody.
XX
PS   Disclosure; Page 21-23; 85pp; English.
XX
CC   The present invention relates to a method for effecting rapid improvement
CC   of cognition in a subject having a condition or disease related to the
CC   Abeta peptide. The method comprises administering an anti-Abeta antibody.
CC   The method is useful for treating cognitive impairments associated with
CC   Abeta peptide including those involved in Alzheimer's disease, Down's
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CC   syndrome, cerebral amyloid angiopathy, certain vascular dementia, and
CC   certain forms of mild cognitive impairment. The anti-Abeta antibody is
CC   useful for preparing a medicament for effecting rapid improvement in
CC   cognition in a subject having Alzheimer's disease, Down's syndrome,
CC   cerebral amyloid angiopathy, or mild cognitive impairment. The present
CC   sequence represents a preferred heavy chain for a humanised 266 antibody
XX
SQ   Sequence 442 AA;

  Query Match            46.9%;  Score 1267.5;  DB 6;  Length 442;
  Best Local Similarity  59.1%;  Pred. No. 1.7e-62;
  Matches  274;  Conservative   26;  Mismatches   69;  Indels   95;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNS---------NQIKILGNQGSF--LTKGPSKL 76
              | : | :: |:| ||          |             ||  :||   :    ||   :
Db         11 LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: :|: | |      :|: ||:  | |                |: |     |
Db         71 S-RDNAKNTLYLQMN------SLRAEDTAVYYC-----------------ASGD---YWG 103

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |   :|: |     |||   :|  |:  ||             : ::||
Db        104 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 163

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                 |: | |  | |    |:|       |||||||
Db        164 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 217

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 277

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 337

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 397

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        398 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 91
ABB80109
ID   ABB80109 standard; protein; 442 AA.
XX
AC   ABB80109;
XX
DT   13-JUN-2003  (first entry)
XX
DE   Heavy chain.
XX
KW   Complementarity determining region; CDR; humanised; mouse; 266; light;
KW   heavy; variable; domain; antibody; preclinical; clinical;
KW   Alzheimer's disease; epitope; amyloid beta peptide; Abeta;
KW   central nervous system; plasma.
XX
OS   Homo sapiens.
OS   Mus musculus.
XX
PN   WO2003015617-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026321.
XX
PR   17-AUG-2001; 2001US-0313221P.
PR   17-AUG-2001; 2001US-0313224P.
PR   23-OCT-2001; 2001US-0334987P.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM,  Demattos R,  Bales KR,  Cummins DJ,  Paul SM;
XX
DR   WPI; 2003-278505/27.
XX
PT   Diagnosing preclinical or clinical Alzheimer's disease in a subject by
PT   administering an antibody which specifically binds an epitope.
XX
PS   Disclosure; Page 15-16; 64pp; English.
XX
CC   The sequences given in AAG80104-09 represent preferred antibodies of the
CC   invention. This sequence represents the preferred heavy chain. The
CC   humanised antibody of the invention may be used for diagnosing
CC   preclinical or clinical Alzheimer's disease. The antibody specifically
CC   binds an epitope, preferably the amyloid beta peptide (Abeta). The
CC   antibodies sequester Abeta from its bound, circulating form in blood and
CC   alter clearance of soluble and bound forms of Abeta in central nervous
CC   system and plasma. The antibodies specifically bind an epitope
CC   representing amino acids 13-28 of the Abeta molecule
XX
SQ   Sequence 442 AA;

  Query Match            46.9%;  Score 1267.5;  DB 6;  Length 442;
  Best Local Similarity  59.1%;  Pred. No. 1.7e-62;
  Matches  274;  Conservative   26;  Mismatches   69;  Indels   95;  Gaps   13;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNS---------NQIKILGNQGSF--LTKGPSKL 76
              | : | :: |:| ||          |             ||  :||   :    ||   :
Db         11 LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI 70

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: :|: | |      :|: ||:  | |                |: |     |
Db         71 S-RDNAKNTLYLQMN------SLRAEDTAVYYC-----------------ASGD---YWG 103

Qy        137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS----------- 172
              |   :|: |     |||   :|  |:  ||             : ::||
Db        104 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 163

Qy        173 --QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                 || ||                 |: | |  | |    |:|       |||||||
Db        164 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 217

Qy        213 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
              ||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 277

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 337

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 397

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        398 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 441


RESULT 92
ABB81109
ID   ABB81109 standard; protein; 470 AA.
XX
AC   ABB81109;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Anti-tissue factor (TF) heavy chain fragment.
XX
KW   Immunoglobulin; promoter; cytostatic; antiinflammatory; immunomodulator;
```

```
KW   neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
KW   TF.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /note= "STII signal sequence TIR-1"
FT   Protein         24. .470
FT                   /note= "anti-tissue factor heavy chain"
XX
PN   WO200261090-A2.
XX
PD   08-AUG-2002.
XX
PF   13-DEC-2001; 2001WO-US048691.
XX
PR   14-DEC-2000; 2000US-0256164P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Simmons LC,  Klimowski L,  Reilly DE,  Yansura DG;
XX
DR   WPI; 2002-619253/66.
DR   N-PSDB; ABN86645.
XX
PT   New polynucleotide comprising first and second promoter-cistron pairs,
PT   useful for diagnosing, treating or preventing diseases associated with
PT   abnormal expression and/or activity of antigens such as inflammatory
PT   disorders.
XX
PS   Disclosure; Fig 20A-C; 104pp; English.
XX
CC   The invention provides a polynucleotide, which encodes an immunoglobulin
CC   (Ig), comprising a first or second promoter-cistron pair consisting of a
CC   first or second promoter and cistron, respectively. The first cistron of
CC   the first promoter-cistron pair comprises a first translational
CC   initiation region (TIR-L) operably linked to a nucleic acid sequence
CC   encoding an Ig light chain and the second cistron of the second promoter-
CC   cistron pair comprises a second translational initiation region (TIR-H)
CC   operably linked to a nucleic acid sequence encoding an Ig heavy chain.
CC   Upon expression of the polynucleotide in a prokaryotic host cell, light
CC   and heavy chains are folded and assembled to form a biologically active
CC   Ig. The antibody of the invention is useful for diagnosing, treating or
CC   preventing diseases or conditions associated with abnormal expression and
CC   /or activity of one or more antigen molecules e.g. lymphoid malignancies,
CC   inflammatory, angiogenic, immunologic, neuronal, glial, astrocytal,
CC   hypothalamic or other glandular disorders. The present sequence
CC   represents the amino acid sequence of an anti-tissue factor (TF) heavy
CC   chain fragment of the cistron vector paTF50
XX
SQ   Sequence 470 AA;

  Query Match             46.9%;  Score 1266;  DB 5;  Length 470;
  Best Local Similarity   58.8%;  Pred. No. 2.2e-62;
  Matches  275;  Conservative   26;  Mismatches   69;  Indels   98;  Gaps   14;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILG-NQGSFLTKGPSKLNDRA 80
              | : | :: |:| ||    |    ||      |    : ::   ||:  |    |  |||
Db         34 LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA 91

Qy         81 -----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-- 133
                  :|: : : | |      :|: ||:  | |                        ||
Db         92 TISADNSKNTAYLQMN------SLRAEDTAVYYCA-----------------RDTAAYF 127

Qy        134 -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------- 172
                 ||   :|: |     |||   :|  |:  ||             : ::||
Db        128 DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 187

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                     || ||                  |: | |  | |    |:|       |||
Db        188 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 241

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        242 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 301

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 361

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||
Db        362 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 421

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469


RESULT 93
ABP72748
ID   ABP72748 standard; protein; 470 AA.
XX
AC   ABP72748;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Anti-tissue factor antibody heavy chain.
XX
KW   CD18; antibody; heavy chain; pxTF-7T3FL; immunosuppressive.
XX
OS   Unidentified.
OS   Escherichia coli.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "heat stable enterotoxin II (STII) signal"
FT   Protein         24. .470
FT                   /note= "Heavy chain"
XX
PN   WO2003018771-A2.
XX
PD   06-MAR-2003.
XX
PF   26-AUG-2002; 2002WO-US027220.
XX
PR   27-AUG-2001; 2001US-0315209P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Andersen DC,  Simmons LC;
XX
DR   WPI; 2003-278654/27.
DR   N-PSDB; ABZ82072.
XX
PT   Producing an antibody for treating cancer or autoimmune diseases by
PT   culturing the host cell under suitable conditions so that the light chain
PT   and heavy chain are expressed in a sequential fashion.
XX
PS   Claim 56; Fig 10; 73pp; English.
XX
CC   The present sequence is that of an anti-tissue factor (TF) antibody heavy
CC   chain including a heat stable enterotoxin II (STII) secretion signal.
CC   This recombinant heavy chain is produced by host cells transformed with
CC   claimed vector pxTF-7T3FL (see ABZ82072). The plasmid contains 2
CC   translational units that temporally separate the transcription of the
CC   antibody light (see ABP72747) and heavy chains. Expression of the light
CC   chain is under the control of the phoA promoter, while expression of the
CC   heavy chain is under the control of the inducible TacII promoter. In an
CC   example from the invention, Escherichia coli 60H4 was transformed with
CC   pxTF-7T3FL. The light chain was expressed initially and secreted into the
CC   periplasmic space. Heavy chain production was then induced by addition of
CC   IPTG A yield of 2.6 +/- 0.3 g/l assembled F(ab')2 was obtained, compared
```

```
CC   with a yield of 1 g/l obtained using a single promoter system. This is an
CC   example of the process of the invention for production of recombinant
CC   antibodies in a host cell system, with temporally separated expression of
CC   the light and heavy chains. Properly assembled, soluble and functional
CC   antibodies (or their fragments) can be produced in high yields for
CC   diagnostic or therapeutic applications, including treatment of cancer or
CC   autoimmune diseases
XX
SQ   Sequence 470 AA;

  Query Match             46.9%;  Score 1266;  DB 6;  Length 470;
  Best Local Similarity   58.8%;  Pred. No. 2.2e-62;
  Matches  275;  Conservative   26;  Mismatches   69;  Indels   98;  Gaps   14;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILG-NQGSFLTKGPSKLNDRA 80
              | : | :: |:| ||    |    ||      |    : ::   ||:  |    |  |||
Db         34 LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA 91

Qy         81 -----DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-- 133
                  :|: : : | |      :|: ||:  | |                    ||
Db         92 TISADNSKNTAYLQMN------SLRAEDTAVYYCA-----------------RDTAAYF 127

Qy        134 -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS------- 172
                ||   :|: |     |||   :|  |:  ||             : ::||
Db        128 DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 187

Qy        173 ------QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
                   || ||                   |: | |  | |    |:|       |||
Db        188 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK 241

Qy        209 SCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 301

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 361

Qy        324 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
              ||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        362 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 421

Qy        384 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469


RESULT 94
AAO14065
ID   AAO14065 standard; protein; 474 AA.
XX
AC   AAO14065;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Heavy chain protein of the monoclonal antibody from clone JA.
XX
KW   HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW   human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW   light chain; central nervous system; CNS; prophylactic therapy; clone JA.
XX
OS   Homo sapiens.
XX
PN   WO200188132-A2.
XX
PD   22-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US014468.
XX
PR   16-MAY-2000; 2000US-0204518P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Hooper DC,  Dietzschold B;
XX
DR   WPI; 2002-062381/08.
DR   N-PSDB; AAK98701.
XX
PT   Novel isolated human monoclonal rabies virus neutralizing antibody useful
PT   for treating individual exposed to rabies virus and for preventing spread
PT   of rabies virus to central nervous system.
XX
PS   Claim 4; Page 23-24; 25pp; English.
XX
CC   This sequence represents the heavy chain protein of the monoclonal
CC   antibody from clone JA. The invention relates to an isolated human
CC   monoclonal rabies virus neutralising antibody (virucide) derived from
CC   cDNA clones encoding the antibody heavy and light chains expressed in
CC   heterologous expression systems and purified away from deleterious
CC   contaminants. The invention provides a fused gene encoding a chimeric
CC   immunoglobulin light chain and a fused gene encoding a chimeric
CC   immunoglobulin heavy chain. The antibody of the invention is useful for
CC   treating an individual exposed to a rabies virus by administering to the
CC   individual a therapeutically effective amount of the antibody, and
CC   preventing a spread of the rabies virus to the central nervous system
CC   (CNS). The antibody of the invention provides a safe and efficacious post
CC   -exposure prophylactic therapy for individuals exposed to a rabies virus
XX
SQ   Sequence 474 AA;

  Query Match             46.9%;  Score 1266;  DB 5;  Length 474;
  Best Local Similarity   59.1%;  Pred. No. 2.2e-62;
  Matches  276;  Conservative   32;  Mismatches   71;  Indels   88;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP 73
              | : | :: |:| ||             |      | ::   |   |:  ::|    ||
Db         30 LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR 86

Qy         74 SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                :: | :|: :|: | |      :|: ||:  | |    :  || ::|  |    |
Db         87 FTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD--- 132

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------- 172
                ||   :|: |     |||   :|  |:  ||             : ::||
Db        133 YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 192

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                   || ||                   |: | |  | |    |:|       ||||
Db        193 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS 246

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 306

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 366

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              |||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||
Db        367 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 426

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473


RESULT 95
ABU08017
ID   ABU08017 standard; protein; 474 AA.
XX
AC   ABU08017;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human monoclonal rabies virus antibody heavy chain, clone JH, protein.
```

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XX
KW   Human; antibody; constant region; monoclonal antibody 57; Mab 57;
KW   variable region; Rabies; neurological disease; infection;
KW   central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
KW   pathogen; vaccine; virucide; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2003016501-A2.
XX
PD   27-FEB-2003.
XX
PF   21-AUG-2002; 2002WO-US026584.
XX
PR   21-AUG-2001; 2001US-0314023P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Hooper DC,  Dietzschold B;
XX
DR   WPI; 2003-278566/27.
DR   N-PSDB; ABX12855.
XX
PT   New recombinant antibody comprising a constant region of Mab 57 linked to
PT   a non-Mab 57 variable region, useful for treating an individual exposed
PT   to a pathogen, e.g. rabies infection.
XX
PS   Example 1; Page 32-33; 38pp; English.
XX
CC   The invention discloses a recombinant antibody comprising a constant
CC   region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
CC   region. Rabies is an acute, neurological disease caused by infection of
CC   the central nervous system with the rabies virus, a member of the
CC   Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
CC   for producing an isolated recombinant antibody by culturing a host cell,
CC   containing a recombinant expression vector comprising the nucleic acid
CC   molecule encoding the antibody, and isolating the recombinant antibody
CC   expressed and treating an individual exposed to a pathogen by
CC   administering to the individual the recombinant antibody. The recombinant
CC   antibodies are useful for preventing (vaccine) and treating an individual
CC   exposed to a pathogen, e.g. rabies infection. They are also useful for
CC   the qualitative and quantitative determination of the rabies virus. The
CC   sequences presented are the antibody protein fragments, the nucleic acids
CC   encoding them or the PCR primers used to construct the recombinant
CC   expression vector
XX
SQ   Sequence 474 AA;

  Query Match             46.9%;  Score 1266;  DB 6;  Length 474;
  Best Local Similarity   59.1%;  Pred. No. 2.2e-62;
  Matches  276;  Conservative   32;  Mismatches   71;  Indels   88;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSFL---TKGP 73
              | : | :: |:| ||             |       | ::  |   |:  ::|    ||
Db         30 LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR 86

Qy         74 SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                :: | :|: :|: | |      :|: ||:  | |    :  || ::|  |    |
Db         87 FTIS-RDNSKNTLYLQMN------SLRAEDTAVYYCA---KDREVTMIVV-LNGGFD--- 132

Qy        134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------- 172
               ||   :|: |     |||   :|  |:  ||             : ::||
Db        133 YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 192

Qy        173 -----QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                  || ||                   |: | |  |:|    |:|       ||||
Db        193 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS 246

Qy        210 CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 264
              |||||||     |||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 306

Qy        265 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 366

Qy        325 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
              |||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||
Db        367 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 426

Qy        385 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473


RESULT 96
ADD25837
ID   ADD25837 standard; protein; 500 AA.
XX
AC   ADD25837;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated protein #181.
XX
KW   Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 398; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
```

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CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 500 AA;

  Query Match             46.9%;  Score 1266;  DB 7;  Length 500;
  Best Local Similarity   56.3%;  Pred. No. 2.3e-62;
  Matches  274;  Conservative   27;  Mismatches   94;  Indels   92;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||         |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |  :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR----------------SPR------ 159
                :|  :| | |  |       ||:|  : |:                  :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 ------------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                       :  :|  ||:|           | |  :||  : |  :       :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 ID-------IVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV 244
              |       :      ||||||||||      ||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSSDQEPKSCDKTHTCPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEV 312

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 372

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 432

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 492

Qy        425 SLSLSPG 431
              |||||||
Db        493 SLSLSPG 499


RESULT 97
ADD25679
ID   ADD25679 standard; protein; 500 AA.
XX
AC   ADD25679;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated protein #114.
XX
KW   Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 240; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
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CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 500 AA;

  Query Match             46.9%;  Score 1266;  DB 7;  Length 500;
  Best Local Similarity   56.3%;  Pred. No. 2.3e-62;
  Matches  274;  Conservative   27;  Mismatches   94;  Indels   92;  Gaps   12;

Qy         23 TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS 82
              :|   ::    |: | :|| ||   |   ||         |:        || |     :
Db         27 SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA 81

Qy         83 RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL---------------- 125
              | |    | :: | |. :: ||: || |    |:       ||
Db         82 RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137

Qy        126 ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR---------------SPR------ 159
                :|  :| | |  |       ||:|  : |:                 :||
Db        138 SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192

Qy        160 -----------GKNIQGGKTLSV-----------SQLELQDSGTWTCTVLQNQKKVEFK 196
                        :  :|  ||:|           | |  :||  : |  :        :
Db        193 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY 252

Qy        197 ID-------IVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV 244
               |       :      ||||||||||     ||||||||||||||||||||||||||||
Db        253 FDVWGTGTTVTVSSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV 312

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 372

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 432

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 492

Qy        425 SLSLSPG 431
              |||||||
Db        493 SLSLSPG 499


RESULT 98
AAR30774
ID   AAR30774 standard; protein; 454 AA.
XX
AC   AAR30774;
XX
DT   25-MAR-2003  (revised)
DT   12-MAY-1993  (first entry)
XX
DE   H52H4-160 murine anti-CD18 antibody heavy chain.
XX
KW   Humanisation; rapid; monoclonal antibody.
XX
OS   Mus musculus.
XX
PN   WO9222653-A1.
XX
PD   23-DEC-1992.
XX
PF   15-JUN-1992;   92WO-US005126.
XX
PR   14-JUN-1991;   91US-00715272.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Carter PJ,  Presta LG;
XX
DR   WPI; 1993-018139/02.
XX
PT   Humanisation of antibodies - by molecular modelling of the variable
PT   domains and alteration by gene conversion mutagenesis.
XX
PS   Disclosure; Fig 6A; 126pp; English.
XX
CC   The sequence is that of the heavy chain of murine anti-CD18 antibody
CC   H52H4-160. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 454 AA;

  Query Match             46.8%;  Score 1265.5;  DB 2;  Length 454;
  Best Local Similarity   59.7%;  Pred. No. 2.2e-62;
  Matches  274;  Conservative   24;  Mismatches   88;  Indels   73;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTK-GPSKLNDRADSRRSL 86
              | | | :|:::|  |     ::  ||   :  | |   | |  | | | |  | |   : :|
Db         11 LVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSHNQRFMDKATL 70

Qy         87 ---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
                     : :::|  |||  | |                ||    |       |   |:
Db         71 AVDKSTSTAYMELRSLTSEDSGIYYC----------ARWRGLNYGFDVRYFDVWGAGTTV 120

Qy        142 TLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS-------------QLE 175
              |: |     |||   :|  |: ||             : ::||
Db        121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180

Qy        176 LQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC- 216
              || ||                 |: | |  | |    |:|       ||||||||||
Db        181 LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP 234

Qy        217 ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 294

Qy        273 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        295 KTKPREEQYNSTTRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 354

Qy        333 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 392
              ||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 414

Qy        393 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||
Db        415 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 453


RESULT 99
AAW85689
ID   AAW85689 standard; protein; 468 AA.
XX
AC   AAW85689;
XX
DT   12-AUG-1999  (first entry)
XX
DE   D9D10 heavy chain fusion protein.
XX
KW   Antibody; humanised; variable region; heavy chain; light chain;
KW   interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW   immune disease; multiple sclerosis; Crohn's disease; skin disorders;
KW   inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
KW   multivalent; ruminant.
XX
OS   Synthetic.
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /note= "D9D10 light chain signal peptide"
FT   Domain          21. .137
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FT                   /note= "Humanised heavy chain variable domain of D9D10"
FT   Domain          138. .467
FT                   /note= "Human IgG1 heavy chain constant domain"
FT   Misc-difference 468
FT                   /note= "Leu added by cloning strategy"
XX
PN   WO9909055-A2.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1998;   98WO-EP005165.
XX
PR   18-AUG-1997;   97EP-00870122.
PR   18-JUN-1998;   98EP-00870139.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Buyse M,  Sablon E;
XX
DR   WPI; 1999-180969/15.
DR   N-PSDB; AAX08631.
XX
PT   New engineered antibodies which bind and neutralise interferon-gamma -
PT   useful for prevention and treatment of septic shock, cachexia, immune
PT   diseases and skin disorders.
XX
PS   Disclosure; Fig 9; 134pp; English.
XX
CC   New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
CC   be used as a medicant, for preventing or treating septic shock, cachexia,
CC   immune diseases including multiple sclerosis and Crohn's disease and skin
CC   disorders including bullous, inflammatory and neoplastic dermatoses. The
CC   antibody is selected from a single chain antibody (scFv), a chimeric
CC   antibody or diabody comprising the humanised variable domain of the
CC   monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody;
CC   or a ruminant antibody. The antibodies are also useful for determining
CC   IFN gamma levels in a sample. Two fusion cDNA genes encoding heavy and
CC   light chain fusion proteins of the humanised D9D10 antibody were
CC   constructed. The light chain comprised cDNA encoding the mouse D9D10
CC   leader sequence, the humanised D9D10 light chain and a human
CC   immunoglobulin kappa light chain constant region. The heavy chain
CC   comprised cDNA encoding the mouse D9D10 light chain leader sequence
CC   followed by the humanised D9D10 heavy chain variable domain and a human
CC   IgG1 heavy chain constant domain in which the C1q-complement binding site
CC   had been mutated. Four overlapping synthetic oligonucleotides (AAX08585-
CC   88) were used to construct the D9D10 light chain leader sequence. This
CC   was then subsequently amplified using two primers (AAX08589, AAX08590) to
CC   generate PCR-V fragment. The humanised heavy chain variable domain was
CC   amplified from pGEM-T-VhH using two primers (AAX08591, AAX08592) to
CC   generate PCR-VI fragment. The two fragments had a base pair overlap and
CC   were fused together using primers (AAX08593, AAX08594) and then cloned
CC   into pGEM-T to give pGEMLdrVHh. The human heavy chain constant domain was
CC   amplified with two primers (AAX08595, AAX08596) and cloned into pGEM-T to
CC   give pGEM-TCh. Two separate PCR amplifications were then performed using
CC   pGEM-T-Ch as a template. The primers used were AAX08598, AAX08599 to
CC   generate PCR-VIII fragment and AAX08597, AAX08600 to generate PCR-IX
CC   fragment. These were then overlapped and fused using primers AAX08599,
CC   AAX08600 and the resulting PCR-X fragment inserted into pGEMLdrVHh to
CC   generate the complete heavy chain fusion DNA in a vector designated
CC   pGEMhD9D10H. For a description of the construction of the light chain
CC   fusion cDNA see GENESEQ records AAX08573-X08584
XX
SQ   Sequence 468 AA;

  Query Match             46.8%;  Score 1265.5;  DB 2;  Length 468;
  Best Local Similarity   57.2%;  Pred. No. 2.3e-62;
  Matches  277;  Conservative   31;  Mismatches   79;  Indels   97;  Gaps   13;

Qy         11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70
              ::: |: |: : ::     | | | :|:::| ||      |     | :|    ||
Db         17 VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L 65

Qy         71 KGPSKLNDRADSRRSLWD-QGNFP-----------LIIKNLKIEDSDTYICEVEDQKEEV 118
                |    :|       : | :| |           | | :|| ||: || |
Db         66 KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC--------- 116

Qy        119 QLLVFGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                       |    : :   ||  |:|: |     |||   :|  |:  ||
Db        117 --------ARRGFYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 168

Qy        167 ---KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQKK 192
                 : ::||                || ||                 |: | |  | |
Db        169 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP 226

Qy        193 VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
                 |:|       ||||||||||      ||||||||||||||||||||||||||||||
Db        227 SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 282

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 342

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              |||||||| ||||||||||||||||||||||:|:|||||||||||||||||||||||||
Db        343 VSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 402

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 462

Qy        428 LSPG 431
              ||||
Db        463 LSPG 466


RESULT 100
AAW85692
ID   AAW85692 standard; protein; 711 AA.
XX
AC   AAW85692;
XX
DT   12-AUG-1999  (first entry)
XX
DE   MoTAbII fusion protein.
XX
KW   Antibody; humanised; variable region; heavy chain; light chain;
KW   interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW   immune disease; multiple sclerosis; Crohn's disease; skin disorders;
KW   inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
KW   multivalent; ruminant.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Mouse_D9D10_light_chain_signal_peptide
FT   Domain          21. .137
FT                   /note= "Humanised heavy chain variable domain of D9D10"
FT   Domain          138. .467
FT                   /note= "Human IgG1 heavy chain constant domain"
FT   Misc-difference 468
FT                   /note= "Leu added by cloning strategy"
FT   Region          469. .472
FT                   /label= Gly(3)Ser_linker
FT   Domain          473. .711
FT                   /label= Humanised)_D9D10_ScFv
XX
PN   WO9909055-A2.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1998;   98WO-EP005165.
XX
PR   18-AUG-1997;   97EP-00870122.
PR   18-JUN-1998;   98EP-00870139.
XX
```

```
PA   (INNO-) INNOGENETICS NV.
XX
PI   Buyse M,  Sablon E;
XX
DR   WPI; 1999-180969/15.
DR   N-PSDB; AAW85692.
XX
PT   New engineered antibodies which bind and neutralise interferon-gamma -
PT   useful for prevention and treatment of septic shock, cachexia, immune
PT   diseases and skin disorders.
XX
PS   Disclosure; Fig 20; 134pp; English.
XX
CC   New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
CC   be used as a medicant, for preventing or treating septic shock, cachexia,
CC   immune diseases including multiple sclerosis and Crohn's disease and skin
CC   disorders including bullous, inflammatory and neoplastic dermatoses. The
CC   antibody is selected from a single chain antibody (scFv), a chimeric
CC   antibody or diabody comprising the humanised variable domain of the
CC   monoclonal mouse anti-IFN gamma antibody D9D10; a multivalent antibody;
CC   or a ruminant antibody. The antibodies are also useful for determining
CC   IFN gamma levels in a sample
XX
SQ   Sequence 711 AA;

  Query Match             46.8%;  Score 1265.5;  DB 2;  Length 711;
  Best Local Similarity   57.2%;  Pred. No. 3.6e-62;
  Matches  277;  Conservative   31;  Mismatches   79;  Indels   97;  Gaps   13;

Qy         11 LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT 70
              ::: |: |: : ::     | | | :|:::| ||       |     | :|    ||
Db         17 VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L 65

Qy         71 KGPSKLNDRADSRRSLWD-QGNFP-----------LIIKNLKIEDSDTYICEVEDQKEEV 118
              |    :|        : | :| |             | | :|| ||: || |
Db         66 KWMGWINTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFC--------- 116

Qy        119 QLLVFGLTANSDTHLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG---------- 166
                    |    : :   ||  |:|: |     |||   :|  |:  ||
Db        117 --------ARRGFYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 168

Qy        167 ---KTLSVS------------QLELQDSG-----------------TWTCTVLQNQKK 192
                 : ::||                || ||                 |: | |  | |
Db        169 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP 226

Qy        193 VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
              |:|       ||||||||||     ||||||||||||||||||||||||||||||
Db        227 SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 282

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 342

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
              |||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||||||
Db        343 VSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 402

Qy        368 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 462

Qy        428 LSPG 431
              ||||
Db        463 LSPG 466


Search completed: August  3, 2004, 13:08:38
Job time : 61.0897 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 3, 2004, 12:51:44 ; Search time 35.157 Seconds
(without alignments)
4594.975 Million cell updates/sec

Title: SEQ8
Perfect score: 2702
Sequence: 1 MNRGVPFRHLLLVLQLALLP.....VISFLLGLGLGVACVLARTR 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 125 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1273	47.1	470	4	Q7Z5W1	Q7z5w1 homo sapien
2	1260.5	46.7	482	4	Q7Z351	Q7z351 homo sapien
3	1255.5	46.5	469	4	Q7Z7P5	Q7z7p5 homo sapien
4	1252	46.3	509	4	Q8NF17	Q8nf17 homo sapien
5	1213	44.9	679	4	Q96PQ8	Q96pq8 homo sapien
6	1180.5	43.7	521	4	Q8N4Y9	Q8n4y9 homo sapien
7	1156.5	42.8	354	4	Q86TT2	Q86tt2 homo sapien
8	1151	42.6	473	4	Q8TC63	Q8tc63 homo sapien
9	912	33.8	337	6	Q95M34	Q95m34 equus cabal
10	884	32.7	470	11	Q7TMK1	Q7tmk1 mus musculu
11	867.5	32.1	437	11	Q9R1A4	Q9r1a4 mus musculu
12	858.5	31.8	469	11	Q8R3V9	Q8r3v9 mus musculu
13	848.5	31.4	463	11	Q99LC4	Q99lc4 mus musculu
14	846	31.3	468	11	Q99L31	Q99l31 mus musculu
15	833.5	30.8	473	11	Q9D8L4	Q9d8l4 mus musculu
16	823.5	30.5	473	11	Q99L25	Q99l25 mus musculu
17	809.5	30.0	473	11	Q91Z05	Q91z05 mus musculu
18	808.5	29.9	474	11	Q8R3H6	Q8r3h6 mus musculu
19	767	28.4	397	6	O09261	O09261 cercopithec
20	767	28.4	397	6	O09262	O09262 cercopithec
21	767	28.4	397	6	O09263	O09263 cercopithec
22	767	28.4	397	6	Q95NE9	Q95ne9 cercopithec
23	763	28.2	397	6	O09259	O09259 cercopithec
24	763	28.2	397	6	O09260	O09260 cercopithec
25	758	28.1	397	6	O02805	O02805 cercopithec
26	746	27.6	457	6	Q8HZT7	Q8hzt7 saimiri sci
27	745	27.6	457	6	Q8HZT8	Q8hzt8 callithrix
28	601.5	22.3	455	6	Q9XS78	Q9xs78 delphinapte
29	557.5	20.6	474	6	P79355	P79355 felis silve
30	467	17.3	457	11	Q61396	Q61396 mus musculu
31	436.5	16.2	433	11	O55054	O55054 mus musculu
32	400	14.8	86	6	O77596	O77596 mandrillus
33	400	14.8	86	6	O77597	O77597 mandrillus
34	397	14.7	86	6	O77594	O77594 cercopithec
35	397	14.7	86	6	O77599	O77599 theropithec
36	395.5	14.6	613	4	Q96EY0	Q96ey0 homo sapien
37	395	14.6	86	6	O77595	O77595 cercocebus
38	392	14.5	86	6	O77598	O77598 papio sp. (
39	389.5	14.4	613	4	Q8WUK1	Q8wuk1 homo sapien
40	389.5	14.4	614	4	Q96GA6	Q96ga6 homo sapien
41	389.5	14.4	618	4	Q96AA6	Q96aa6 homo sapien
42	388	14.4	86	6	O77601	O77601 lophocebus
43	385	14.2	597	4	Q9BU10	Q9bu10 homo sapien
44	385	14.2	597	4	Q9BQB8	Q9bqb8 homo sapien
45	385	14.2	597	4	Q96BB9	Q96bb9 homo sapien
46	383	14.2	86	6	O77600	O77600 lophocebus
47	381	14.1	614	11	Q7TMT6	Q7tmt6 mus musculu
48	380	14.1	588	4	Q8WUX4	Q8wux4 homo sapien
49	373.5	13.8	613	11	Q8VCX7	Q8vcx7 mus musculu
50	366.5	13.6	375	4	Q86TT1	Q86tt1 homo sapien
51	357	13.2	71	4	Q13969	Q13969 homo sapien
52	345.5	12.8	587	13	Q7T0R1	Q7t0r1 xenopus lae
53	336	12.4	478	4	Q7Z379	Q7z379 homo sapien
54	322.5	11.9	492	4	Q7Z374	Q7z374 homo sapien
55	315.5	11.7	484	11	Q99LA6	Q99la6 mus musculu
56	314.5	11.6	487	11	Q99KA4	Q99ka4 mus musculu
57	313.5	11.6	489	11	Q8VCX4	Q8vcx4 mus musculu
58	312	11.5	416	4	Q9NPP6	Q9npp6 homo sapien
59	311	11.5	481	11	Q91WT1	Q91wt1 mus musculu
60	311	11.5	482	11	Q8K172	Q8k172 mus musculu
61	307	11.4	482	11	Q91X92	Q91x92 mus musculu
62	305.5	11.3	99	6	Q29027	Q29027 sus scrofa
63	305	11.3	486	11	Q91Z07	Q91z07 mus musculu
64	304	11.3	488	11	Q8K0F2	Q8k0f2 mus musculu
65	301.5	11.2	684	13	Q90544	Q90544 ginglymosto
66	300.5	11.1	480	11	Q91XE1	Q91xe1 mus musculu
67	300.5	11.1	494	4	Q96K68	Q96k68 homo sapien
68	298.5	11.0	481	11	Q91WT3	Q91wt3 mus musculu
69	297.5	11.0	484	11	Q8VEA0	Q8vea0 mus musculu
70	297.5	11.0	487	11	Q80ZI7	Q80zi7 mus musculu
71	297.5	11.0	496	4	Q96KX8	Q96kx8 homo sapien
72	295	10.9	493	4	Q8NCL6	Q8ncl6 homo sapien
73	293	10.8	488	11	Q91WR1	Q91wr1 mus musculu
74	290	10.7	499	4	Q8N5K4	Q8n5k4 homo sapien
75	287.5	10.6	496	4	Q96DK0	Q96dk0 homo sapien
76	286.5	10.6	426	11	Q9DCD9	Q9dcd9 mus musculu
77	286.5	10.6	479	11	Q91WP5	Q91wp5 mus musculu
78	284.5	10.5	479	11	Q7TMK4	Q7tmk4 mus musculu
79	284.5	10.5	481	11	Q8VCV5	Q8vcv5 mus musculu
80	284	10.5	497	4	Q8WY24	Q8wy24 homo sapien
81	281.5	10.4	384	4	Q9UP60	Q9up60 homo sapien
82	281	10.4	479	11	Q99M22	Q99m22 mus musculu
83	280.5	10.4	99	6	Q29028	Q29028 sus scrofa
84	273.5	10.1	500	4	Q9BRV0	Q9brv0 homo sapien
85	270	10.0	480	11	Q8K0Z4	Q8k0z4 mus musculu
86	193.5	7.2	573	4	Q8WU38	Q8wu38 homo sapien
87	189	7.0	482	13	Q90WB5	Q90wb5 anas platyr
88	186	6.9	268	13	Q90524	Q90524 ginglymosto
89	183.5	6.8	130	11	Q9D8W4	Q9d8w4 mus musculu

90	183.5	6.8	234	4	Q8N355	Q8n355 homo sapien
91	183.5	6.8	235	11	Q99M11	Q99m11 mus musculu
92	182	6.7	236	4	Q7Z3Y4	Q7z3y4 homo sapien
93	181.5	6.7	398	4	Q7Z3B9	Q7z3b9 homo sapien
94	181.5	6.7	955	4	Q8NFP4	Q8nfp4 homo sapien
95	181	6.7	379	11	Q8BLX5	Q8blx5 mus musculu
96	181	6.7	397	11	Q8BFX8	Q8bfx8 mus musculu
97	176.5	6.5	233	4	Q96I69	Q96i69 homo sapien
98	176.5	6.5	259	13	Q90530	Q90530 ginglymosto
99	176.5	6.5	739	6	Q28260	Q28260 canis famil
100	176.5	6.5	739	11	Q63669	Q63669 rattus norv
101	174.5	6.5	885	6	Q8HYV1	Q8hyv1 sus scrofa
102	174.5	6.5	886	6	Q8HYV2	Q8hyv2 sus scrofa
103	174	6.4	233	4	Q8N5F4	Q8n5f4 homo sapien
104	174	6.4	236	4	Q96E61	Q96e61 homo sapien
105	173	6.4	233	4	Q8TBC9	Q8tbc9 homo sapien
106	173	6.4	234	4	Q7Z473	Q7z473 homo sapien
107	172.5	6.4	234	4	Q7Z2U7	Q7z2u7 homo sapien
108	172.5	6.4	238	7	Q9MXA2	Q9mxa2 aulonocara
109	171.5	6.3	257	13	Q90536	Q90536 ginglymosto
110	171	6.3	731	6	Q8SPI6	Q8spi6 macropus eu
111	170	6.3	237	13	Q90545	Q90545 ginglymosto
112	170	6.3	482	4	Q8NF20	Q8nf20 homo sapien
113	168.5	6.2	811	5	Q9VNP2	Q9vnp2 drosophila
114	168.5	6.2	1011	5	Q24273	Q24273 drosophila
115	167.5	6.2	267	13	Q90529	Q90529 ginglymosto
116	167.5	6.2	739	6	Q9GKR3	Q9gkr3 bos taurus
117	167	6.2	105	11	Q99JC1	Q99jc1 mus musculu
118	166	6.1	239	4	Q8NEK0	Q8nek0 homo sapien
119	166	6.1	240	4	Q8WUK3	Q8wuk3 homo sapien
120	165	6.1	106	4	Q8TCJ5	Q8tcj5 homo sapien
121	165	6.1	237	4	Q8WUK4	Q8wuk4 homo sapien
122	165	6.1	237	4	Q8WTU6	Q8wtu6 homo sapien
123	165	6.1	650	6	Q9GKR2	Q9gkr2 bos taurus
124	164	6.1	8081	5	Q7Z120	Q7z120 caenorhabdi
125	163.5	6.1	584	4	Q9Y3Y8	Q9y3y8 homo sapien

ALIGNMENTS

```
RESULT 1
Q7Z5W1
ID   Q7Z5W1      PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match            47.1%;  Score 1273;  DB 4;  Length 470;
  Best Local Similarity  59.3%;  Pred. No. 2.9e-96;
  Matches  274;  Conservative   25;  Mismatches   81;  Indels   82;  Gaps   11;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFLTKGPSK---LND 78
              | : | :: |:| ||     :   ||      |    :  :| |     |  |
Db         30 LVQPGGSLRLSCVASGFTLNNYDMHWVRQGIGKGLEWVSKIGTAGDRYYAGSVKGRFTIS 89

Qy         79 RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
              | ::: ||: | |      :|:: |:  | |               |  |      : ||
Db         90 RENAKDSLYLQMN------SLRVGDAAVYYC----------ARGAGRWAPLGAFDIWGQG 133

Qy        139 LTLTLESPPGSSPSVQCRSPRGKNIQGG------------KTLSVS------------ 172
               :|: |    |||   :|  |:  ||             : ::||
Db        134 TMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 193

Qy        173 QLELQDSG-----------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH 214
                 || ||                 |: | |  | |    |:|       |||||||||
Db        194 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTH 247

Qy        215 TC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269
              ||     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 307

Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 367

Qy        330 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 427

Qy        390 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||||||||||||||||||||||||||
Db        428 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469


RESULT 2
Q7Z351
ID   Q7Z351      PRELIMINARY;      PRT;   482 AA.
AC   Q7Z351;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686N02209.
GN   DKFZP686N02209.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538118; CAD98026.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   482 AA;  52852 MW;  EDA75F1901D1A034 CRC64;
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  Query Match           46.7%;  Score 1260.5;  DB 4;  Length 482;
  Best Local Similarity  56.4%;  Pred. No. 3.3e-95;
  Matches  279;  Conservative   29;  Mismatches   96;  Indels   91;  Gaps   15;

Qy         10 LLLVLQLALL-------PAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW------K 54
              |  | :|||            |  ||  : | :: |:| ||         ||      |
Db          5 LTWVFVVALLRGVQCQAQVVESGGSVV--QPGRSLRLSCIASGFSFSGSAMHWLRQIPGK 62

Qy         55 NSNQIKIL---GNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV 111
                 : ::   ||   :      :     |: :||       | : :|   |:  | |
Db         63 GLEWVAVISYDGNHKLYSDSVKGRFTISRDNSKSL-----LFLHVNSLTSADTAIYYCAR 117

Qy        112 EDQKEEVQLLVFGLT------ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQG 165
              :   :     :|||      :  ||    |:  |: : |     |||   :|  |:  |
Db        118 DFHSKTTS--IFGLIPLYFYYSAMDT---WGRGTTVIVSSASTKGPSVFPLAPSSKSTSG 172

Qy        166 G-------------KTLSVS-------------QLELQDSG-----------------T 181
              |             : ::||             || ||                     |
Db        173 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT 232

Qy        182 WTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTL 236
              : | |  | |    |:|       ||||||||||     ||||||||||||||||||||
Db        233 YICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL 286

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 346

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG 406

Qy        357 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEG 466

Qy        417 LHNHYTQKSLSLSPG 431
              |||||||||||||||
Db        467 LHNHYTQKSLSLSPG 481
```

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RESULT 3
Q7Z7P5
ID   Q7Z7P5      PRELIMINARY;      PRT;   469 AA.
AC   Q7Z7P5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051328; AAH51328.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;
```

```
  Query Match           46.5%;  Score 1255.5;  DB 4;  Length 469;
  Best Local Similarity  56.5%;  Pred. No. 8.1e-95;
  Matches  274;  Conservative   34;  Mismatches   84;  Indels   93;  Gaps   12;

Qy         16 LALLPAATQGNKVV--------LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGS 67
              | |: |||      |         : | | :|:|:|     |:  ::: : : | :    |
Db          8 LFLVAAATGARPQVHLVQSGAEVKKPGASVKLSC-----KTSGYNFSSYDLIWVRQAPGQ 62

Qy         68 FL------------TKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQK 115
              |              ||    |   |             :: :  ::|: :|:  : |  : :
Db         63 GLEWMGWISAHNGDTKYARKFQGRVTMTTDTSATTSY-MEFRSLRSDDTALFYCATKSR- 120

Qy        116 EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG--------- 166
                  |   : |:    ||   :|: |     |||   :|  |:  ||
Db        121 --------GQVGDFDS---WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK 169

Qy        167 ----KTLSVS-------------QLELQDSG-----------------TWTCTVLQNQK 191
                  : ::||               || ||                 |: | |  | |
Db        170 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHK 227

Qy        192 KVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTC 246
                |:|       ||||||||||     ||||||||||||||||||||||||||||||
Db        228 PSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 283

Qy        247 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 343

Qy        307 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 403

Qy        367 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 463

Qy        427 SLSPG 431
              |||||
Db        464 SLSPG 468
```

```
RESULT 4
Q8NF17
ID   Q8NF17      PRELIMINARY;      PRT;   509 AA.
AC   Q8NF17;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FLJ00385 protein (Fragment).
GN   FLJ00385.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT   "The nucleotide sequence of a long cDNA clone isolated from human
RT   spleen.";
```

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RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090464; BAC03445.1; -.
DR   PIR; A45874; A45874.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   509 AA;  56111 MW;  089498D8076E863C CRC64;

  Query Match             46.3%;  Score 1252;  DB 4;  Length 509;
  Best Local Similarity   55.0%;  Pred. No. 1.8e-94;
  Matches  262;  Conservative   30;  Mismatches   66;  Indels  118;  Gaps   11;

Qy         52 HWKNSNQIKILGNQGSFL--------------------TKGPSKLNDRADSRRS------ 85
              ||       |  |||:                        |||||       || :
Db         28 HWTLPGPSWIDKNQGASAPWAQLCPTPQSHGAISLAASTKGPSVFPLAPCSRSTSGGTAA 87

Qy         86 ----------------LWDQG-------NFPLIIKNLKIED-------------SDTYICE 110
                            |: |        || ::::  :                : || |
Db         88 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCN 147

Qy        111 VE--------DQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKN 162
              |        |:: |::          ||         : ::||   |  :|  |:
Db        148 VNHKPSNTKVDKRVELK-----TPLGDTTHTCPRCPEPKSCDTPP---PCPRCPEPK--- 196

Qy        163 IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCP-APEPKSCDKTHTC----- 216
                              :|                 |||  |||||||    |
Db        197 --------------------SCDTPP------------PCPRCPEPKSCDTPPPCPRCPA 224

Qy        217 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 276
              |||||||||||||||||||||||||||||||||||||||||||||:| ||||||||||||||
Db        225 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 284

Qy        277 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 336
              ||||:|||:|||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        285 REEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTL 344

Qy        337 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 396
              ||||:|:|||||||||||||||||||||||:||||||| ||||:|||||||||||||||
Db        345 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLT 404

Qy        397 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
              ||||||||||:||||||||||| :||||||||| |||:|:|||||||||||||||
Db        405 VDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPELQLEESCAEAQDGELDGLWTT 460


RESULT 5
Q96PQ8
ID   Q96PQ8      PRELIMINARY;      PRT;   679 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hu Z., Garen A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF272774; AAK58686.2; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000152; Asx_hydroxyl_S.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002383; GLA_blood.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00010; EGFBLOOD.
DR   PRINTS; PR00001; GLABLOOD.
DR   SMART; SM00181; EGF; 2.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00069; GLA; 1.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
SQ   SEQUENCE   679 AA;  75552 MW;  0B0023AE70A067A1 CRC64;

  Query Match             44.9%;  Score 1213;  DB 4;  Length 679;
  Best Local Similarity   96.2%;  Pred. No. 4.3e-91;
  Matches  228;  Conservative    1;  Mismatches    2;  Indels    6;  Gaps    2;

Qy        201 PCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 254
              | | : ||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        442 PFPGSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 501

Qy        255 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 561

Qy        315 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 621

Qy        375 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 678


RESULT 6
Q8N4Y9
ID   Q8N4Y9      PRELIMINARY;      PRT;   521 AA.
AC   Q8N4Y9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033178; AAH33178.1; -.
DR   PIR; A60764; A60764.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   521 AA;  57156 MW;  2AC7D22E72D6CAA2 CRC64;

  Query Match             43.7%;  Score 1180.5;  DB 4;  Length 521;
  Best Local Similarity   51.5%;  Pred. No. 1.4e-88;
  Matches  261;  Conservative   40;  Mismatches   85;  Indels  121;  Gaps   13;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQ--GSFLTKGPSKLND--------- 78
              | : | :: |:| ||       : :   |    | :  | | :|      :
Db         30 LVQPGGSLRLSCAASGFIVSDHYVEWVRQAPGKGPEWVGCFRSKAHKSTTEYAASVKGRF 89

Qy         79 ---RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-L 134
                 | ||: |:  | |     :|| :|:  | | | | :                | :  :
Db         90 TILRDDSKNSVHLQMN------SLKTDDTAVYYC-VRDLEG---------AGKYDWYFDI 133

Qy        135 QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------------KTLSVS--------- 172
               |: : :|: |     |||   :|  ::  ||             : ::||
Db        134 WGRGILVTVSSASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 193

Qy        173 ----QLELQDSG-----------------TWTCTV------LQNQKKVEFKIDI----- 199
                   || ||                  |:|| |       :  |:|| |  :
Db        194 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTH 253

Qy        200 ----------------------------VPCP-APEPKSCDKTHTC-----PELLGGPS 224
                                         |||  |||||||     |     ||||||||
Db        254 TCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPS 313

Qy        225 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 284
              ||||||||||||||||||||||||||||||||:| ||||||||||||||||||:|||
Db        314 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNST 373

Qy        285 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT 344
              :|||||||||||||||||||||||||||||||||||| ||||||||||||||:|:|
Db        374 FRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMT 433

Qy        345 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 404
              |||||||||||||||||||||||:||||||| ||||:||||||||||||||||||||||
Db        434 KNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQ 493

Qy        405 GNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||:|||||||||||| :||||||||||
Db        494 GNIFSCSVMHEALHNRFTQKSLSLSPG 520


RESULT 7
Q86TT2
ID   Q86TT2      PRELIMINARY;      PRT;   354 AA.
AC   Q86TT2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens
DE   (Human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Genoscope;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX248278; CAD62606.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   354 AA;  39125 MW;  23B80BF4D2B87A92 CRC64;

  Query Match             42.8%;  Score 1156.5;  DB 4;  Length 354;
  Best Local Similarity   61.2%;  Pred. No. 7.7e-87;
  Matches  232;  Conservative   25;  Mismatches   45;  Indels   77;  Gaps    9;

Qy         87 WDQG-------NFPLIIKNLKIED-------------SDTYICEVE--------DQKEEV 118
              |: |         || ::::  :                : || | |         |:: |:
Db         18 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVEL 77

Qy        119 QLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQD 178
              :           ||          : ::||    |  :|  |:
Db         78 K-----TPLGDTTHTCPRCPEPKSCDTPP---PCPRCPEPK------------------ 110

Qy        179 SGTWTCTVLQNQKKVEFKIDIVPCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKP 232
                :|              |||  |||||||    |     ||||||||||||||||
Db        111 ----SCDTPP-----------PCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKP 154

Qy        233 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292
              |||||||||||||||||||||||||:| ||||||||||||||||||||:|||||||
Db        155 KDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLT 214

Qy        293 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 352
              |||||||||||||||||||||||||||||||||| ||||||||||||||:|:|||||||||
Db        215 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC 274

Qy        353 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412
              |||||||||||||||:||||||| ||||:|||||||||||||||||||||:|||||
Db        275 LVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV 334

Qy        413 MHEALHNHYTQKSLSLSPG 431
              ||||||| :||||||||||
Db        335 MHEALHNRFTQKSLSLSPG 353


RESULT 8
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
DR   GO; GO:0005507; F:copper ion binding; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00196; COPPER_BLUE; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

  Query Match             42.6%;  Score 1151;  DB 4;  Length 473;
  Best Local Similarity   53.7%;  Pred. No. 3.3e-86;
  Matches  262;  Conservative   33;  Mismatches  105;  Indels   88;  Gaps   16;

Qy         8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW------ 53
             :||   | |   |         | :   | |   |: |||| |     |  ::|
Db         9 KHLWFFLLLVAAPRWVLSRLQLQESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQP 68

Qy        54 --KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV 111
               |    |  :   |: :   || |  |      :  : :| | : ::   |:  | |
Db        69 PGKGLEWIGTINFSGN-MYYSPS-LRSRVTMSADM-SENSFYLKLDSVTAADTAVYYCAA 125

Qy       112 EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSS--PSVQCRSPRGKNI------ 163
                      || |  |    |  ||: ::::  |  | |  |   |     ::
Db       126 GH-------LVMGFGA----HWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCL 174

Qy       164 --------------QGGKTLSVSQLE--LQDSG------------------TWTCTV--- 186
                            |  |  |      || ||                  |:|| |
Db       175 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHK 234

Qy       187 ---LQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPE 243
                 :  |:|| |    |||     ||      || ||||||||||||||||||||||||
Db       235 PSNTKVDKRVESKYG-PPCP-----SC----PAPEFLGGPSVFLFPPKPKDTLMISRTPE 284

Qy       244 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 303
             ||||||||| |||||:|||||||||||||||||||||:||||||||||||||||||||||
Db       285 VTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKE 344

Qy       304 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 363
             |||||||| ||: |||||||||||||||||||||||::|:||||||||||||||||||||
Db       345 YKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA 404

Qy       364 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 423
             ||||||||||||||||||||||||||||||:|||||||||:|||||||||||||||||||
Db       405 VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQ 464

Qy       424 KSLSLSPG 431
             |||||| |
Db       465 KSLSLSLG 472


RESULT 9
Q95M34
ID   Q95M34      PRELIMINARY;      PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunogobulin gamma 1 heavy chain constant region (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300675; CAC44624.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   337 AA;  37438 MW;  A60BF2B01DEFD1F6 CRC64;

  Query Match             33.8%;  Score 912;  DB 6;  Length 337;
  Best Local Similarity   59.1%;  Pred. No. 9.8e-67;
  Matches  179;  Conservative   40;  Mismatches   60;  Indels   24;  Gaps    7;

Qy       142 TLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVEFK 196
             :| |   : |||         :|     |:| :    : |||     | |:       ||
Db        45 SLTSGVHTFPSV---------LQSSGFYSLSSMVTVPASTWTSETYICNVVHAAS--NFK 93

Qy       197 ID--IVPCPAPEPKSCD--KTHTC--PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 250
             :|  | | |    | ||  |   |  ||||||||||:||| |||||||:|||||||||||
Db        94 VDKRIEPIPDNHQKVCDMSKCPKCPAPELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVD 153

Qy       251 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 310
             || |:|:||||||:|||||  | |:|:|||:|||||||||| : |||||:|||:||||:|
Db       154 VSQENPDVKFNWYMDGVEVRTATTRPKEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNN 213

Qy       311 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 370
             :||| |||:||:| ||: :||||| | |  |||:|::||:||||| ||| :| :||:|||
Db       214 QALPQPIERTITKTKGRSQEPQVYVLAPHPDELSKSKVSVTCLVKDFYPPEINIEWQSNG 273

Qy       371 QP--ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
             ||  |  | ||    |||||:||||||:||::|||||  |:| |||||||||||||::|
Db       274 QPELETKYSTTQAQQDSDGSYFLYSKLSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSK 333

Qy       429 SPG 431
             :||
Db       334 NPG 336


RESULT 10
Q7TMK1
ID   Q7TMK1      PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match             32.7%;  Score 884;  DB 11;  Length 470;
  Best Local Similarity   43.0%;  Pred. No. 3.2e-64;
  Matches  196;  Conservative   61;  Mismatches  129;  Indels   70;  Gaps   12;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL 86
              | | | :|:::| ||          ||   :  | |    |    : | :  | :   : :|
Db         30 LVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSYNQKFKGKATL 89

Qy         87 W---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL 143
                  : : :|  |||  | |       :      |     |   : |   |:|:
Db         90 TVDKSSSTAYMELNSLTSEDSAVYYC--------ARYYYSGSYWYFD---VWGAGTTVTV 138

Qy        144 ESPPGSSPSVQ-----CRSPRGKNI-----------------------QGGKTL----- 169
                |   ::|||      |    | ::                      | :|:
Db        139 SSATTTAPSVYPLVPGCGDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ 198

Qy        170 ----SVSQLELQDSGTW-----TCTVLQNQKKVEFKIDI---VPCPAPEPKSCDKTHTCP 217
                  |:| |    | ||      | |      | |    :| |:  | |     :||
Db        199 SGFYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----SCP 253

Qy        218 --ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 275
                :|||||||:|||||| |||| ||:||||||||| :||:|  :|:||  ||| | |:
Db        254 PGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQ 313

Qy        276 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 335
              ||| |||||:|||| | : ||||: |||:||||:|||||||||:|||| ||: : |||||
Db        314 PREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYT 373

Qy        336 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 395
              :|| |::::| :|||||||  |:   |:|||| ||: | :|| |||:|||||::||||||
Db        374 IPPPREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKL 433

Qy        396 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||   | || :|:|||:|||||||:|||:|| |||
Db        434 TVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPG 469


RESULT 11
Q9R1A4
ID   Q9R1A4      PRELIMINARY;      PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Gamma1 heavy chain of Mab7 (Fragment).
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   PIR; B45837; B45837.
DR   PDB; 1CQK; 11-SEP-99.
DR   PDB; 1I9I; 25-DEC-02.
DR   PDB; 1KCU; 11-MAY-02.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
FT   NON_TER       1      1
FT   NON_TER     437    437
SQ   SEQUENCE   437 AA;  48142 MW;  5C3A7BB3EE7D697C CRC64;

  Query Match             32.1%;  Score 867.5;  DB 11;  Length 437;
  Best Local Similarity   41.6%;  Pred. No. 6.6e-63;
  Matches  188;  Conservative   66;  Mismatches  123;  Indels   75;  Gaps   11;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              | | | :::|:| ||      |   |      | |    || : |    |    | :::
Db         10 LVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGIIYYTDSVKGRFTIY 69

Qy         88 ---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLE 144
                 |:    | : :|: ||:  | |                  |  |     |    :|:
Db         70 KDKDRNILSLQMSSLRSEDTAMYYC----------------ARGDYSAYWGPGTLVTVS 112

Qy        145 SPPGSSPSVQCRSP----------------------------RGKNIQGGKTL-SVSQL 174
                :   : |||   :|                          |    |  |  :| |
Db        113 AAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 172

Qy        175 ELQ--------DSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL 219
                :|          | ||     || |    :  ||: ||    |   :|  |   | ||:
Db        173 DLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGC-KPCIC----TVPEV 227

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
                |||:|||||| | |: ||:||||||:| :||||:|:|:|| |||| |:|:||||
Db        228 ---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE 284

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              |:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|: |||||:||
Db        285 QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 344

Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              :::: |::|||||::  |:| || ||||: ||||  ||| | |::|:|||:|:|||| | |
Db        345 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQK 404

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              | |: || |:|||:|| ||||:|:|:|| |||
Db        405 SNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPG 436


RESULT 12
Q8R3V9
ID   Q8R3V9      PRELIMINARY;      PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-4.
```

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
DR   PIR; B45837; B45837.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51976 MW;  534793F155D05457 CRC64;

  Query Match             31.8%;  Score 858.5;  DB 11;  Length 469;
  Best Local Similarity   41.6%;  Pred. No. 4e-62;
  Matches  192;  Conservative   67;  Mismatches  120;  Indels   83;  Gaps   14;

Qy         30 LGKKGDTVELTCTAS------------QKKSIQFHWKNSNQIKILG--NQGSFLTKGPS 74
              | : | :: |:| ||             |    : |  |  : |    ||
Db         30 LVQPGGSLRLSCAASGFTFTDYYMSWVRQPPGKALEWLGFIRNKANGYTTEYSASVKGRF 89

Qy         75 KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL 134
               :: | :|:  |: | |       |: ||| || |   |::            :  :
Db         90 TIS-RDNSQSILYLQMN------ALRAEDSATYYC-ARDRRSSYYY-------SGTSFAY 134

Qy        135 QGQSLTLTLESPPGSSPSVQCRSP----------------------------RGKNIQG 165
               ||   :|: :   : |||   :|                            |   |
Db        135 WGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSG 194

Qy        166 GKTL-SVSQLELQ--------DSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKS 209
              |  :| | :|           | ||     || |     :  ||: ||    |   :|
Db        195 VHTFPAVLQSDLYTLSSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRDCGC-KPCI 253

Qy        210 CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269
              |    | ||:    |||:|||||| | |: ||:||||||:| :||||:|:|:|| |||
Db        254 C----TVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEV 306

Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
              | |:||||||:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|:
Db        307 HTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPK 366

Qy        330 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 389
              |||||:|| :::: |::|||||::  |:| || ||| |||| ||| | |::|:|||:
Db        367 APQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSY 426

Qy        390 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |:|||| | || |: || |:|||:|| ||||:|:|||| |||
Db        427 FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 468


RESULT 13
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   PIR; B45837; B45837.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

  Query Match             31.4%;  Score 848.5;  DB 11;  Length 463;
  Best Local Similarity   40.6%;  Pred. No. 2.6e-61;
  Matches  191;  Conservative   63;  Mismatches  111;  Indels  105;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS------------QKKSIQFHWKNSNQIKILGNQG----SFLTKG 72
              | : | :| |:| ||            |:      |      :|    |    |   ||
Db         30 LARPGASVRLSCKASGYTFTGYGVSWVKQRTGQGLEWVG----EIYPGSGNTYYSEKFKG 85

Qy         73 PSKL-NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANS-- 129
                : |  |:: |   :          : :|  |||  | |                  | |
Db         86 KATLTTDKSSSTAYMH--------LSSLTSEDSAVYFC-----------------ARSSY 120

Qy        130 ---DTHLLQGQSLTLTLESPPGSSPSVQCRSP--------------------------- 158
                 |     ||   :|: :   : |||   :|
Db        121 YSYDLFAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW 180

Qy        159 -RGKNIQGGKTL-SVSQLELQ--------DSGTW-----TCTVLQ--NQKKVEFKIDIVP 201
               |   | |  :| | :|           | ||     || |    :  ||: ||
Db        181 NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRD 240

Qy        202 CPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 261
              |   :|  |    | ||:    |||:|||||| | |: ||:||||||:| :||||:|:
Db        241 CGC-KPCIC----TVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFS 292

Qy        262 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 321
              |:|| |||| |:|:|||||:|||:| || | ::|||||||||:||:|:: | ||||||||
Db        293 WFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTI 352

Qy        322 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 381
              || ||:|: |||||:|| :::: |::|||||::  |:| || ||| |||| ||| | |
Db        353 SKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQP 412

Qy        382 VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ::|:|||:|:|||| | || |: || |:|||:|| ||||:|:|||| |||
Db        413 IMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 462


RESULT 14
Q99L31
ID   Q99L31      PRELIMINARY;      PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   PDB; 2AP2; 24-NOV-99.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
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DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   468 AA;  51661 MW;  96352328B3332ADB CRC64;

  Query Match             31.3%;  Score 846;  DB 11;  Length 468;
  Best Local Similarity   42.7%;  Pred. No. 4.3e-61;
  Matches  198;  Conservative   55;  Mismatches  123;  Indels   88;  Gaps   15;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG----------SFLTKGPSKLN 77
              | : | :|:|:|||||    |    ||     :|    ||            ||   |
Db         30 LVRPGASVKLSCTASGFNIKDSLMHW-----VKQRPEQGLEWIGWIDPEDGETKYAPKFQ 84

Qy         78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQ 137
              |:|          : | : :|  ||:  | |         : |::|       :   ||
Db         85 DKATITADTSSNTAY-LQLSSLTSEDTAIYYC--------ARNLLYG-----GYYDYWGQ 130

Qy        138 SLTLTLESPPGSSPSVQ-----CRSPRGKNIQGG----------KTL------------- 169
                |:|: |   ::|||       |    | ::  |           ||
Db        131 GTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT 190

Qy        170 --SVSQLELQ--------DSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEP 207
                :| | :|          | ||      || |    :  ||: ||:     | |||   |
Db        191 FPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---P 247

Qy        208 KSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
                |      | ||||||||:|||| || |||| :| |||||||||| :||:|: :|:|: |
Db        248 CKC----PAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNV 303

Qy        268 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
              ||  |:|:   | |||| |||| | : ||||::|||:||||:|||||||||:|||| ||
Db        304 EVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGS 363

Qy        328 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
                | |||| |||  :|:|| ||:|||:|  | | || ||| :||: | ||| | |||||||
Db        364 VRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDG 423

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |:|:|||| |:|  | : | :||||:|| ||||:| || | :||
Db        424 SYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 467


RESULT 15
Q9D8L4
ID   Q9D8L4      PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1810060O09Rik protein.
GN   IGH-1 OR 1810060O09RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   PIR; S26746; S26746.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

  Query Match             30.8%;  Score 833.5;  DB 11;  Length 473;
  Best Local Similarity   40.0%;  Pred. No. 4.6e-60;
  Matches  185;  Conservative   67;  Mismatches  131;  Indels   79;  Gaps   11;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-SFLTK-----GPSKLNDRADSR 83
              | | | :|:::| ||       ::    | :|    ||  :: |     | :  |::   :
Db         30 LVKPGASVKISCKASGYTFTDYY---INWVKQRPGQGLEWIGKIGPGSGSTYYNEKFKGK 86

Qy         84 RSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              :|         : : :|  |||  | |                        : |    ||
Db         87 ATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY------------DYDWFAYWGQGTL 133

Qy        141 LTLESPPGSSPSVQ-----CRSPRGKNI------------------------------- 163
              :|: :   ::|||       |    | ::
Db        134 VTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPA 193

Qy        164 ---QGGKTLSVSQLELQDSGTW-----TCTV------LQNQKKVEFKIDIVPCPAPEPKS 209
                 |  ||| |      | ||     || |       :  ||:| :: |   | | |
Db        194 LLQSGLYTLSSS--VTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPLKE 251

Qy        210 CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269
              |     |:|||||||:|||| || |||| :| |||||||| :||:|: :|:|: |||
Db        252 CPPC-AAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEV 310

Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
              | |:|:   | |||| |||| | : ||||::|||:||||:|:|||:|||||||| :|  |
Db        311 HTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVR 370

Qy        330 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 389
               |||| |||  :|:|| : ||||:: || |::|||:| |||: | ||| |  |||||||:
Db        371 APQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSY 430

Qy        390 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |:|||| | || |::|::|:|||:|| |||| | |::| | |
Db        431 FMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLG 472


RESULT 16
Q99L25
ID   Q99L25      PRELIMINARY;      PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; BC003888; AAH03888.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   473 AA;  52449 MW;  BE9889B7986DA155 CRC64;

  Query Match             30.5%;  Score 823.5;  DB 11;  Length 473;
  Best Local Similarity   41.2%;  Pred. No. 3.1e-59;
  Matches  193;  Conservative   59;  Mismatches  136;  Indels   81;  Gaps   15;

Qy         24 QGNKVVLGKKGDTVELTCTASQKKSIQ--FHWKNSNQIKILGNQG------SFLTKGPSK 75
              |:   | | | :|:::|  |          ||     :|    ||       :   | :|
Db         24 QQSDAELVKPGASVKISCKVSGYTFTDHTIHW-----VKQRPEQGLEWIGYIYPRDGSTK 78

Qy         76 LNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH 132
               |::   : :|         : : :|  |||     |           : :|      :
Db         79 YNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGS------IYYGYGLYYFDY 132

Qy        133 LLQGQSLTLTLESPPGSSPSVQ-----CRSPRGKNIQGG----------KTL-------- 169
                 ||  |:|: |   ::|||       |     | ::  |           ||
Db        133 --WGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS 190

Qy        170 -------SVSQLELQ--------DSGTW-----TCTVLQ--NQKKVEFKID-----IVPC 202
                    :| | :|          | ||      || |     :  ||: ||:      | ||
Db        191 SGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPC 250

Qy        203 PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
              |   |  |      | ||||||||:|||| || |||| :| |||||||| :||:|: :|
Db        251 P---PCKC----PAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISW 303

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              :|: |||  |:|:   | |||| |||| | : ||||::|||:||||:|||||||||:|||
Db        304 FVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTIS 363

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | ||  | |||| |||  :|:|| ||:|||:|  | | || ||| :||: | ||| | ||
Db        364 KPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPV 423

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||:|:|||| |:|  | : | :||||:|| ||||:| || | :||
Db        424 LDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 472


RESULT 17
Q91Z05
ID   Q91Z05      PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

  Query Match             30.0%;  Score 809.5;  DB 11;  Length 473;
  Best Local Similarity   40.1%;  Pred. No. 4.4e-58;
  Matches  188;  Conservative   61;  Mismatches  127;  Indels   93;  Gaps   14;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILG-----NQGSF------LTKGPSKL 76
              | | | : :|:| ||          ||      | |       | ||         ||   :
Db         30 LVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYYADTVKGRFTI 89

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
              : | ::: :|:      | : :|: ||:  | |   |     :                |
Db         90 S-RDNAKNTLF------LQMTSLRSEDTAMYYCARELWLRRID-------------YWG 128

Qy        137 QSLTLTLESPPGSSPSVQ-----CRSPRGKNI-------------------QGGKTLSV- 171
                 |:|: |   : |||       |     | ::                    | : ||
Db        129 QGTTITVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVH 188

Qy        172 ------------SQLELQDSGTW-----TCTVLQ--NQKKVEFKID-------IVPCPA 204
                         |      | ||      ||:|     :    |: |::        | |||
Db        189 TFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCP- 247

Qy        205 PEPKSCDKTHTC--PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 262
                | : | |  | | ||||||:|||  || |||| ||:|||||||| :||:|: :|
Db        248 ----PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISW 303

Qy        263 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 322
              :|: |||| |:|:   | |||| |||| | : ||||::|||:||||:|| ||:|||:|||
Db        304 FVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTIS 363

Qy        323 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 382
              | ||  | |||| |||  ::|::  ||||||| || | ||:||| |||  | ||| | ||
Db        364 KIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPV 423

Qy        383 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||:|:|||| :  |:|:: : |||:| || | :|: :|::| |||
Db        424 LDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG 472


RESULT 18
Q8R3H6
ID   Q8R3H6      PRELIMINARY;      PRT;   474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
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DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

  Query Match             29.9%;  Score 808.5;  DB 11;  Length 474;
  Best Local Similarity   39.4%;  Pred. No. 5.3e-58;
  Matches  193;  Conservative   63;  Mismatches  125;  Indels  109;  Gaps   17;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTASQ---KKSIQFHWKN------SNQIKILGN- 64
              |: || :  :     | | | :|:::| ||     ||    | |          :: :|
Db         20 QVQLLQSGPE-----LVKPGASVKISCRASGYAFSKS----WMNWVKRRPGKGLEWIGRI 70

Qy         65 ---------QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQK 115
                      | |  :| :||    |  :       | : :|  |||  | |  :
Db         71 FPGDGDTHYSGKF--QGKAKLTADKSSVTAF-------LQLTSLTSEDSAVYFCARDSD- 120

Qy        116 EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ-----CRSPRGKNI------- 163
                    :|     |     ||  |:|: |   : |||       |    | ::
Db        121 -------YG-----DYFDDWGQGATVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVK 168

Qy        164 ------------QGGKTLSV--------------SQLELQDSGTW-----TCTVLQ--NQ 190
                         |  : ||               |      | ||     ||:|    :
Db        169 GYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASS 228

Qy        191 KKVEFKID-------IVPCPAPEPKSCDKTHTC--PELLGGPSVFLFPPKPKDTLMISRT 241
               |: |::       | |||      | : | |  | | ||||||:|||  || |||| |
Db        229 TTVDKKLEPSGPISTINPCP-----PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLT 283

Qy        242 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 301
              |:|||||||| :||:|: :|:|: |||| |:|:   | |||| |||| | : ||||::|
Db        284 PKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSG 343

Qy        302 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD 361
              ||:||||:|| ||:|||:|||| ||  | |||| |||  ::|::  ||||||| || | |
Db        344 KEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGD 403

Qy        362 IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY 421
              |:||| |||  | ||| | |||||||:|:|||| :  |:|:: : |||:| || | |:|
Db        404 ISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYY 463

Qy        422 TQKSLSLSPG 431
               :|::| |||
Db        464 LKKTISRSPG 473


RESULT 19
O09261
ID   O09261      PRELIMINARY;      PRT;   397 AA.
AC   O09261;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 (Fragment).
GN   CD4.
OS   Cercopithecus sabaeus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=60711;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
DR   EMBL; AF001225; AAB60872.1; -.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     397    397
SQ   SEQUENCE   397 AA;  43945 MW;  80C963B92A868CD3 CRC64;

  Query Match             28.4%;  Score 767;  DB 6;  Length 397;
  Best Local Similarity   85.5%;  Pred. No. 1.1e-54;
  Matches  148;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              |||||||||||||| |||  : |||||||||||||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
              ||| | :|||||||||:|||||||::||||:|||||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              ||||||:||||||||||:|||| ||| |||||||||| |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNMVEFKIDIV 173


RESULT 20
O09262
ID   O09262      PRELIMINARY;      PRT;   397 AA.
AC   O09262;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 (Fragment).
GN   CD4.
OS   Cercopithecus tantalus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=60712;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
DR   EMBL; AF001221; AAB60868.1; -.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     397    397
SQ   SEQUENCE   397 AA;  43954 MW;  CF7F2F5D82335B0D CRC64;

  Query Match             28.4%;  Score 767;  DB 6;  Length 397;
  Best Local Similarity   85.5%;  Pred. No. 1.1e-54;
  Matches  148;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              |||||||||||||| |||  : |||||||||||||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
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              ||| | :||||||||||:|||||||::||||:||||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              ||||||:||||||||||||:|||| ||| |||||||||| |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV 173


RESULT 21
O09263
ID   O09263      PRELIMINARY;      PRT;   397 AA.
AC   O09263;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 (Fragment).
GN   CD4.
OS   Cercopithecus tantalus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=60712;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
DR   EMBL; AF001222; AAB60869.1; -.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     397    397
SQ   SEQUENCE   397 AA;  43994 MW;  A3CD031535A51524 CRC64;

  Query Match             28.4%;  Score 767;  DB 6;  Length 397;
  Best Local Similarity   85.5%;  Pred. No. 1.1e-54;
  Matches  148;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              |||||||||||||| ||| : |||||||||||||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
              ||| | :||||||||||:|||||||::||||:||||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              ||||||:||||||||||||:|||| ||| |||||||||| |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV 173


RESULT 22
Q95NE9
ID   Q95NE9      PRELIMINARY;      PRT;   397 AA.
AC   Q95NE9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 (Fragment).
GN   CD4.
OS   Cercopithecus pygerythrus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=60710;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
DR   EMBL; AF001227; AAB60874.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     397    397
SQ   SEQUENCE   397 AA;  43946 MW;  21C3E30882ABFBC0 CRC64;

  Query Match             28.4%;  Score 767;  DB 6;  Length 397;
  Best Local Similarity   85.5%;  Pred. No. 1.1e-54;
  Matches  148;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              |||||||||||||| ||| : |||||||||||||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
              ||| | :||||||||||:|||||||::||||:||||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              ||||||:||||||||||||:|||| ||| |||||||||| |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV 173


RESULT 23
O09259
ID   O09259      PRELIMINARY;      PRT;   397 AA.
AC   O09259;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 (Fragment).
GN   CD4.
OS   Cercopithecus sabaeus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=60711;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
DR   EMBL; AF001223; AAB60870.1; -.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
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DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     397    397
SQ   SEQUENCE   397 AA;  43881 MW;  7CE39AD0F8506C81 CRC64;

  Query Match             28.2%;  Score 763;  DB 6;  Length 397;
  Best Local Similarity   85.0%;  Pred. No. 2.3e-54;
  Matches  147;  Conservative   11;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              |||||||||||||| |||| : |||||||||||||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQKTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
              ||| | :|||||||||||:|||||||:::|||:|||||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKEEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              ||||||:||||||||||||:|||| ||| |||||||| | |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCNVSQDQNTVEFKIDIV 173


RESULT 24
O09260
ID   O09260      PRELIMINARY;      PRT;   397 AA.
AC   O09260;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 (Fragment).
GN   CD4.
OS   Cercopithecus sabaeus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=60711;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
DR   EMBL; AF001224; AAB60871.1; -.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     397    397
SQ   SEQUENCE   397 AA;  43882 MW;  478BB277E992EE89 CRC64;

  Query Match             28.2%;  Score 763;  DB 6;  Length 397;
  Best Local Similarity   85.0%;  Pred. No. 2.3e-54;
  Matches  147;  Conservative   11;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              |||||||||||||| |||| : |||||||||||||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQKTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
              ||| | :|||||||||||:|||||||:::|||:|||||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKEEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              ||||||:||||||||||||:|||| ||| |||||||| | |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCNVSQDQNTVEFKIDIV 173


RESULT 25
O02805
ID   O02805      PRELIMINARY;      PRT;   397 AA.
AC   O02805; O77593;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
GN   CD4.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=98017879; PubMed=9379478;
RA   Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA   Corbet S., Barre-Sinoussi F., Allan J.S.;
RT   "Relation between phylogeny of African green monkey CD4 genes and
RT   their respective simian immunodeficiency virus genes.";
RL   J. Med. Primatol. 26:120-128(1997).
RN   [2]
RP   SEQUENCE OF 80-165 FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (Primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 3 C2-LIKE DOMAINS.
DR   EMBL; AF001226; AAB60873.1; -.
DR   EMBL; AF057380; AAC25124.1; -.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Lipoprotein; Palmitate; Repeat.
FT   NON_TER       1      1
FT   DOMAIN       <1    370       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    371    391       POTENTIAL.
FT   DOMAIN      392   >397       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       <1     98       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       99    176       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      177    290       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN      291    347       IG-LIKE C2-TYPE DOMAIN 3.
FT   CARBOHYD     15     15       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     30     30       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    269    269       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    298    298       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     14     82       BY SIMILARITY.
FT   DISULFID    128    157       BY SIMILARITY.
FT   DISULFID    301    343       BY SIMILARITY.
FT   LIPID       392    392       S-palmitoyl cysteine (By similarity).
FT   LIPID       395    395       S-palmitoyl cysteine (By similarity).
FT   NON_TER     397    397
```

```
SQ   SEQUENCE   397 AA;  43980 MW;  F74C42E22B196155 CRC64;

  Query Match             28.1%;  Score 758;  DB 6;  Length 397;
  Best Local Similarity   85.0%;  Pred. No. 6e-54;
  Matches  147;  Conservative   10;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
              ||||||||||||||| |||| : |||||||| |||| |||||||| ||| || |||:|||
Db          1 VVLGKKGDTVELTCNASQKTTTQFHWKNSNQTKILGKQGSFLTKGSSKLRDRIDSRKSLW 60

Qy         88 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP 147
              ||| | :|||||||||:|||||||::|||||:|||||||||||||||||||||||||||
Db         61 DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP 120

Qy        148 GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
              |||||||||||||| |:|||| ||| |||||||||| |:|  ||||||||
Db        121 GSSPSVKCRSPRGKNIQVGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV 173


RESULT 26
Q8HZT7
ID   Q8HZT7      PRELIMINARY;      PRT;   457 AA.
AC   Q8HZT7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Lymphocyte antigen CD4.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22174698; PubMed=12186836;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 Infection of New World Monkey Cells Occurs
RT   Primarily at the Stage of Virus Entry.";
RL   J. Exp. Med. 196:431-445(2002).
DR   EMBL; AF452617; AAN14533.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   457 AA;  50899 MW;  B164DA89E70C575A CRC64;

  Query Match             27.6%;  Score 746;  DB 6;  Length 457;
  Best Local Similarity   40.3%;  Pred. No. 7.1e-53;
  Matches  210;  Conservative   56;  Mismatches  149;  Indels  106;  Gaps   20;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              || |:|||||||||||||||| |  |||||||: ||| |  | ||:: |||| |::||
Db          1 MNGGIPFRHLLLVLQLALLPAATHGKTVVLGKKGEVVELPCETSLKKNVPFHWKTSDRIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||| |  |:|:| ||| || ||:|| ||:|:|||:||: :||||:||||||| :||||:|
Db         61 ILGVQNYFVTRGQSKLTDRIDSKRSSWDRGSFPLLIKDARIEDSETYICEVESKKEEVEL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
               ||||||| |||||||||||||||||||:| ||||| |:| ||||||| : |||
Db        121 QVFGLTANPDTHLLQGQSLTLTLESPPGSSPSVECTSPRGKRIRGRKTLSVSQLGIPDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFP-PKPKDTLMIS 239
              || ||| |: : | |:|:||     :  |     |  :  |    | ||     :|| |
Db        181 TWKCTVFQHLELV-FEINIVVLAFQQASS-----TVYKKEGEQVEFSFPLAFAAETLTGS 234

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 299
                                 :  |     :   | :     :| | : | |  |
Db        235 G-----------------ELCW-----QAERASSSKSWITFNLTKQEVYVKLVT----- 266

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 359
                :: | ::  |    |:  |:::|  |      :||                 :||
Db        267 --QDPKLRMGKK---LPLHLTLAQALPQYAGSGNFTL----------------ALKG--- 302

Qy        360 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
                                ||          |      | | :    | |: :| |
Db        303 ----------------KT--------GKLHQEVNLVVMRVTQLQNNL-TCEVWGP---- 332

Qy        420 HYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDP-PRASALPAPPTGSALPDPQTASAL 478
                |   | ||  |:|:   |:    |   :|  :| | |       :|  | : :   ||
Db        333 --TSPKLMLS--LKLENQEAKVSKRE-KAVWVLNPEPGAWQCLLSDSGQVLLESK-FEAL 386

Qy        479 P--DPPAASALPAALAVISFLLGL----GLGV-ACVLARTR 512
              |   ||     |  | |:  : ||    |||:  ||  | |
Db        387 PTRSPPVQ---PMVLIVLGGVAGLLAFTGLGIFLCVRCRHR 424


RESULT 27
Q8HZT8
ID   Q8HZT8      PRELIMINARY;      PRT;   457 AA.
AC   Q8HZT8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Lymphocyte antigen CD4.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22174698; PubMed=12186836;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 Infection of New World Monkey Cells Occurs
RT   Primarily at the Stage of Virus Entry.";
RL   J. Exp. Med. 196:431-445(2002).
DR   EMBL; AF452616; AAN14532.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   457 AA;  50878 MW;  718CFDB78D97F59B CRC64;

  Query Match             27.6%;  Score 745;  DB 6;  Length 457;
  Best Local Similarity   40.0%;  Pred. No. 8.6e-53;
  Matches  210;  Conservative   52;  Mismatches  149;  Indels  114;  Gaps   21;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              || |:|||| |||||||||| | | |  |||||||: ||| |  | || :||||| |||||
Db          1 MNGGIPFRHSLLVLQLALLIAVTHGKTVVLGKKGEMVELPCETSLKKKLQFHWKTSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||| |||||||| ||| :| ||::| ||:|:|||||:|:::|||:|||||| :||||:|
Db         61 ILGIQGSFVTKGQSKLANRIDSKQSSWDRGSFPLIIRNVQVEDSETYICEVESKKEEVEL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
               ||||| | ||||||||||||||||||||:| ||||| |:| ||| :||||:||||
Db        121 QVFGLTVNPDTHLLQGQSLTLTLESPPGSSPSVECMSPRGKTIRGMKTLFMSQLEIQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISR 240
              || ||| |: : | |||:||     :  |     |  :  |    | ||       :
Db        181 TWKCTVSQHLELV-FKINIVVLAFQQASS-----TVYKKEGEQVEFSFP-------LAFA 227
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Qy        241 TPEVT-----CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 295
Db        228 AEQLTGSGELC--------------W-----QAERASSSESWITFNLTNQEVCVKLVTQ 267

Qy        296 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 355
Db        268 DPKLR--------MGKKLPFHL----------------TLPQALPQYA-GSGNFTLALK 301

Qy        356 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
Db        302 G--------------------KT--------GKLHQEVKLVVMRATQLQNNL-TCEVWGP 332

Qy        416 ALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDPP-RASALPAPPTGSALPDPQT 474
Db        333 ------TSPKLVLS--LKLENQEAKVSKRE-KAVWVLNPEVGAWQCLLSDSGQVLLESK- 382

Qy        475 ASALP--DPPAASALPAALAVISFLLGL----GLGV-ACVLARTR 512
Db        383 VEVLPTWSPPVQ---PMALIVLGGVAGLLVFTGLGIFLCVRCRHR 424
```

RESULT 28
Q9XS78
ID Q9XS78 PRELIMINARY; PRT; 455 AA.
AC Q9XS78;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=99216435; PubMed=10199913;
RA Romano T.A., Ridgway S.H., Felten D.L., Quaranta V.;
RT "Molecular cloning and characterization of CD4 in an aquatic mammal,
RT the white whale Delphinapterus leucas.";
RL Immunogenetics 49:376-383(1999).
DR EMBL; AF071799; AAD23738.1; -.
DR HSSP; P01730; 1WIQ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TCAg.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 455 AA; 50499 MW; AA532FD4411AA5D1 CRC64;

Query Match 22.3%; Score 601.5; DB 6; Length 455;
Best Local Similarity 40.8%; Pred. No. 5.6e-41;
Matches 155; Conservative 43; Mismatches 107; Indels 75; Gaps 9;

```
Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
Db          1 MDPRTSLRHLFLVLQLVMLPAGTQGKKVVLGKAGELAELPCKASQNKSLFFSWKNSYQTK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
Db         61 ILGRHGYFWHKGASNLHSRVESKINLWDQGSFPLVIKDLEVPDSGTYICEVEDKKIEVEL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
Db        121 QVFRLTASSDTRLLLGQSLTLTLEGPSGSNPSVQWKGPGNKRKNEAKSLSLPQVGLQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISR 240
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Db        181 TWTCTVSQAQQTLVFNKHILVLAFQEVSS-----TVYAKEGEQMNFSFP---------- 224

Qy        241 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL- 299
Db        225 --------LTFGDENLSGELSWL----------QAKGNSS----------PESWIT 252

Qy        300 ----NG--------KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL---- 343
Db        253 FKLNNGKVTVGKARKDLKLRMS-KAL--PLHLTLPQALPQYAGSGNLTLNLTKGKLYQEV 309

Qy        344 -------TKNQVSLTCLVKG 356
Db        310 NLVVMRVTKSPNSLTCEVLG 329
```

RESULT 29
P79355
ID P79355 PRELIMINARY; PRT; 474 AA.
AC P79355;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD4 antigen precursor.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazawa T.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92165316; PubMed=1537604;
RA Norimine J., Miyazawa T., Kawaguchi Y., Tohya Y., Kai C., Mikami T.;
RT "A cDNA encoding feline CD4 has a unique repeat sequence downstream of
RT the V-like region.";
RL Immunology 75:74-79(1992).
DR EMBL; AB000483; BAA19124.1; -.
DR HSSP; P01730; 1WIQ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TCAg.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 474 POTENTIAL.
SQ SEQUENCE 474 AA; 52243 MW; D946DD4BEAED00EC CRC64;

Query Match 20.6%; Score 557.5; DB 6; Length 474;
Best Local Similarity 55.3%; Pred. No. 2.5e-37;
Matches 121; Conservative 30; Mismatches 49; Indels 19; Gaps 3;

```
Qy          1 MNRGVPFRHLLLVLQLALLPAAT-QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI 59
Db          1 MNQGAVFRHLLLVLQLVMLKAAVPQGKEVVLGKAGGTAELPCQASQKKYMTFTWRLSSQV 60

Qy         60 KILGNQGSFL-TKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV 118
Db         61 KILESQHSSLCLTGSSKLKTRFESKKILWDQGSFPLVIKSLQVADSGIYTCEVENKKREV 120

Qy        119 QLLVFGLTANSD----------------THLLQGQSLTLTLESPPGSSPSVQCRSPRGK 161
Db        121 ELLVFGLTAKVDPSGSGGSSSSSTSTSTSIYLLQGQSLTLTLESPSSSNPSVQWKGPGNK 180

Qy        162 NIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
Db        181 SKSGVHSLSLSQLELQESGTCTCTVSQSQKTLVFNTNIL 219
```

```
RESULT 30
Q61396
ID   Q61396      PRELIMINARY;      PRT;   457 AA.
AC   Q61396;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell differentiation antigen.
GN   CD4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88041159; PubMed=2823269;
RA   Gorman S.D., Tourvieille B., Parnes J.R.;
RT   "Structure of the mouse gene encoding CD4 and an unusual transcript in
RT   brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).
DR   EMBL; M17080; AAA37402.1; -.
DR   EMBL; M17076; AAA37402.1; JOINED.
DR   EMBL; M17077; AAA37402.1; JOINED.
DR   EMBL; M17078; AAA37402.1; JOINED.
DR   EMBL; M17079; AAA37402.1; JOINED.
DR   HSSP; P01730; 1WBR.
DR   MGD; MGI:88335; Cd4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   457 AA;  51368 MW;  24AB19EDA285B5D0 CRC64;

  Query Match             17.3%;  Score 467;  DB 11;  Length 457;
  Best Local Similarity   52.3%;  Pred. No. 6.7e-30;
  Matches  103;  Conservative   32;  Mismatches   56;  Indels    6;  Gaps    5;

Qy          1 MNRGVPFRH-LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI 59
              | | :  |  |||:|||: | | ||   :||||:|:: || | :||||    | || |:|
Db          1 MCRAISLRRLLLLLLLQLSQLLAVTQEKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR 60

Qy         60 KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
              ||||  |   | :|  ||:  || ||::  |::|:|||||  ||:||| |||||:|::||
Db         61 KILGQHGKGVLIRGGSPSQF-DRFDSKKGAWEKGSFPLIINKLKMEDSQTYICELENRKE 119

Qy        117 EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE 175
              ||:| || :| :  | ||||||||||:|    |:|  :|:  :|| : | | ||:| |
Db        120 EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR 179

Qy        176 LQDSGTWTCTVLQNQKK 192
              :|||  | |||  :|||
Db        180 VQDSDFWNCTVTLDQKK 196


RESULT 31
O55054
ID   O55054      PRELIMINARY;      PRT;   433 AA.
AC   O55054;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T4 surface glycoprotein (Fragment).
GN   CD4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88097446; PubMed=3501122;
RA   Maddon P.J., Molineaux S.M., Maddon D.E., Zimmerman K.A., Godfrey M.,
RA   Alt F.W., Chess L., Axel R.;
RT   "Structure and expression of the human and mouse T4 genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Maddon P.J., Molineaux S.M., Maddon D.E., Zimmerman K.A., Godfrey M.,
RA   Alt F.W., Chess L., Axel R.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF045882; AAC01764.1; -.
DR   HSSP; P01730; 1WBR.
DR   MGD; MGI:88335; Cd4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     433    433
SQ   SEQUENCE   433 AA;  48590 MW;  AB19330750A8499A CRC64;

  Query Match             16.2%;  Score 436.5;  DB 11;  Length 433;
  Best Local Similarity   53.2%;  Pred. No. 2e-27;
  Matches   92;  Conservative   29;  Mismatches   47;  Indels    5;  Gaps    4;

Qy         24 QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-SFLTKG--PSKLNDRA 80
              ||  :||||:|:: || | :||||    | || |:| ||||  |   | :|  ||:  ||
Db          1 QGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQRKILGQHGKGVLIRGGSPSQF-DRF 59

Qy         81 DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLT 140
              ||::  |::|:|||||  ||:||| |||||:|::||||:| || :| :  | ||||||||
Db         60 DSKKGAWEKGSFPLIINKLKMEDSQTYICELENRKEEVELWVFKVTFSPGTSLLQGQSLT 119

Qy        141 LTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKK 192
              |||:|    |:|  :|:  :|| : | | ||:| | :|||  | |||  :|||
Db        120 LTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLRVQDSDFWNCTVTLDQKK 172


RESULT 32
O77596
ID   O77596      PRELIMINARY;      PRT;    86 AA.
AC   O77596;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Mandrillus sphinx (Mandrill) (Papio sphinx).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Mandrillus.
OX   NCBI_TaxID=9561;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
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CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057386; AAC25130.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20    >86       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49     78       BY SIMILARITY.
FT   NON_TER      86     86
SQ   SEQUENCE   86 AA;  9406 MW;  2BD97A9EE19582AB CRC64;

  Query Match             14.8%;  Score 400;  DB 6;  Length 86;
  Best Local Similarity   89.4%;  Pred. No. 2.1e-25;
  Matches   76;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:||||||||||||||||:||||||||||||||||||:||||||||||||
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| |||||||||| |:||
Db         61 RTLSVPQLERQDSGTWTCTVSQDQK 85


RESULT 33
O77597
ID   O77597      PRELIMINARY;      PRT;    86 AA.
AC   O77597;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Mandrillus.
OX   NCBI_TaxID=9568;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057387; AAC25131.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20    >86       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49     78       BY SIMILARITY.
FT   NON_TER      86     86
SQ   SEQUENCE   86 AA;  9406 MW;  2BD97A9EE19582AB CRC64;

  Query Match             14.8%;  Score 400;  DB 6;  Length 86;
  Best Local Similarity   89.4%;  Pred. No. 2.1e-25;
  Matches   76;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:||||||||||||||||:||||||||||||||||||:||||||||||||
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| |||||||||| |:||
Db         61 RTLSVPQLERQDSGTWTCTVSQDQK 85


RESULT 34
O77594
ID   O77594      PRELIMINARY;      PRT;    86 AA.
AC   O77594;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Cercopithecus mitis.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=36225;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057381; AAC25125.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20    >86       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49     78       BY SIMILARITY.
FT   NON_TER      86     86
SQ   SEQUENCE   86 AA;  9417 MW;  371CA39EF58182AB CRC64;

  Query Match             14.7%;  Score 397;  DB 6;  Length 86;
  Best Local Similarity   89.4%;  Pred. No. 3.7e-25;
  Matches   76;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:||||||||||||||||||||||||||||||||||:||||||||||||
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              : ||| ||| |||||||||| |:||
Db         61 RILSVPQLERQDSGTWTCTVSQDQK 85


RESULT 35
O77599
ID   O77599      PRELIMINARY;      PRT;    86 AA.
AC   O77599;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Theropithecus gelada (Gelada baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Theropithecus.
OX   NCBI_TaxID=9565;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057389; AAC25133.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20     >86      IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49      78      BY SIMILARITY.
FT   NON_TER      86      86
SQ   SEQUENCE   86 AA;  9420 MW;  2BD97A98574EE9AB CRC64;

  Query Match             14.7%;  Score 397;  DB 6;  Length 86;
  Best Local Similarity   88.2%;  Pred. No. 3.7e-25;
  Matches   75;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:|||||||||||||||:|||||||||||||:||||:||||||||||||
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGTSPSVKCRSPRGKNIQGG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| ||||||||||| |:||
Db         61 RTLSVPQLERQDSGTWTCTVSQDQK 85


RESULT 36
Q96EY0
ID   Q96EY0      PRELIMINARY;      PRT;   613 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67273 MW;  31214203FB8421E7 CRC64;

  Query Match             14.6%;  Score 395.5;  DB 4;  Length 613;
  Best Local Similarity   22.2%;  Pred. No. 7.9e-24;
  Matches  135;  Conservative   83;  Mismatches  206;  Indels  185;  Gaps   19;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI 61
              :||   | |   |         | :   | |  :|: |||| |      ::|    |
Db          2 KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAG 61

Qy         62 LGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYIC------- 109
               | :  |   | | :  |    || ::     :  | | : ::   |:  | |
Db         62 KGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCASQPWEL 121

Qy        110 ----------------------------EVEDQKEEVQLLVFGLTA------------ 127
                                         |:   :   :  |  |
Db        122 PTVGLFYWGQGTLVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSW 181

Qy        128 ----NSD-------------------------THLLQGQS------------------ 138
                  |||                       ::||
Db        182 KYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNVP 241

Qy        139 LTLTLESPPGSSPSVQCR------------------SPR---------GKNIQGGKTLS 170
              | :  | ||  |  | |                  |||          || :  | |
Db        242 LPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTD 301

Qy        171 VSQLELQDSG--------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS 209
                | | ::||                  :|| |  : : : |: :      |:  :
Db        302 QVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDT 359

Qy        210 CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269
              :             ||  ||    :: :::: ::||:| |::  |  |  :|     |
Db        360 AIR------------VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEA 405

Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP- 328
                |   |   |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||
Db        406 VKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVAL 465

Qy        329 REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD- 384
              | || |||:|::|  :   ::|||| || |:|: |:|   |||     | |: |: :
Db        466 HRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEP 525

Qy        385 -SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQD 443
               : | :| :| ||| :  |  |  ::| | |||| |  |:::: |      |    | :
Db        526 QAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-----TEGEVSADE 580

Qy        444 GELDGLWTT 452
                : || |
Db        581 EGFENLWAT 589


RESULT 37
O77595
ID   O77595      PRELIMINARY;      PRT;   86 AA.
AC   O77595;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Cercocebus galeritus chrysogaster.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=75569;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057382; AAC25126.1; -.
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DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20    >86       IG-LIKE C2-TYPE DOMAIN.
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     49     78       BY SIMILARITY.
FT   NON_TER      86     86
SQ   SEQUENCE   86 AA;  9419 MW;  A9D97A9EE19582BE CRC64;

  Query Match             14.6%;  Score 395;  DB 6;  Length 86;
  Best Local Similarity   88.2%;  Pred. No. 5.4e-25;
  Matches   75;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:||||||||||||||:||||||||||||||||||:||||||||||||
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| |||||||| | |:||
Db         61 RTLSVPQLERQDSGTWTCNVSQDQK 85


RESULT 38
O77598
ID   O77598      PRELIMINARY;      PRT;    86 AA.
AC   O77598;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Papio sp. (Baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=61183;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057388; AAC25132.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20    >86       IG-LIKE C2-TYPE DOMAIN.
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     49     78       BY SIMILARITY.
FT   NON_TER      86     86
SQ   SEQUENCE   86 AA;  9433 MW;  A9D97A98574EE9BE CRC64;

  Query Match             14.5%;  Score 392;  DB 6;  Length 86;
  Best Local Similarity   87.1%;  Pred. No. 9.5e-25;
  Matches   74;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:||||||||||||||:||||||||||||||:||||:||||||||||||
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGTSPSVKCRSPRGKNIQGG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| |||||||| | |:||
Db         61 RTLSVPQLERQDSGTWTCNVSQDQK 85


RESULT 39
Q8WUK1
ID   Q8WUK1      PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020240; AAH20240.1; -.
DR   PIR; PL0120; PL0120.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

  Query Match             14.4%;  Score 389.5;  DB 4;  Length 613;
  Best Local Similarity   23.9%;  Pred. No. 2.5e-23;
  Matches  116;  Conservative   77;  Mismatches  167;  Indels  125;  Gaps   16;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |      || | ||  |   |   :|                        ||
Db        162 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 196

Qy         94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL----------QGQSLTLT 142
               :::  |   :   :   :|           :   :| |::           :   | :
Db        197 SVLRGGKYAATSQVLLPSKD----------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 245

Qy        143 LESPPGSSPSVQCR------------------SPR---------GKNIQGGKTLSVSQL 174
              | ||  |  | |                   |||         || :  | |    |
Db        246 AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA 305

Qy        175 ELQDSG--------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT 213
              | ::||                   :|| |  : : : |: :      |:  :  :
Db        306 EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR- 362

Qy        214 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                      ||  ||    :: :::: ::||:| |::  |  |  :|     |
Db        363 ----------VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH 409

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ 332
              |   |  |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     |
Db        410 TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD 469

Qy        333 VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG 387
              || |||:|::|  :   ::|||| || |:|: |:|   |||     | |: |: :  : |
Db        470 VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG 529

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD 447
              :| :| ||| :  |  |  ::| | |||| |  |::::  |      |    | :  :
Db        530 RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-----TEGEVSADEEGFE 584

Qy        448 GLWTT 452
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Db        585 NLWAT 589


RESULT 40
Q96GA6
ID   Q96GA6      PRELIMINARY;      PRT;   614 AA.
AC   Q96GA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009851; AAH09851.1; -.
DR   PIR; S15590; S15590.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000005; HTHAraC.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   614 AA;  67921 MW;  55EF536E77AA9BBB CRC64;

  Query Match             14.4%;  Score 389.5;  DB 4;  Length 614;
  Best Local Similarity   23.9%;  Pred. No. 2.5e-23;
  Matches  116;  Conservative   77;  Mismatches  167;  Indels  125;  Gaps   16;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |       || | ||  |    |   :|                       ||
Db        163 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 197

Qy         94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL-----------QGQSLTLT 142
               :::  |   :   :   :|         :   :| |::           :  | :
Db        198 SVLRGGKYAATSQVLLPSKD-----------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 246

Qy        143 LESPPGSSPSVQCR-------------------SPR---------GKNIQGGKTLSVSQL 174
               | ||  |  |  |                  |||         || :  | |    |
Db        247 AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA 306

Qy        175 ELQDSG--------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT 213
              | ::||                    :|| |  : : : |: :      |:  :  :
Db        307 EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR- 363

Qy        214 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                  ||  ||    :: :::: ::||:| |::  |  |  :|     |
Db        364 -----------VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH 410

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ 332
              |   |   |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     |
Db        411 TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD 470

Qy        333 VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG 387
              || |||:|::|   :   ::|||| || |:|: |:|   |||      | |: |: : : |
Db        471 VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG 530

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD 447
               :| :| ||| :  |  |  ::| | |||| |  |:::: |      |    |:   :
Db        531 RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-----TEGEVSADEEGFE 585

Qy        448 GLWTT 452
                || |
Db        586 NLWAT 590


RESULT 41
Q96AA6
ID   Q96AA6      PRELIMINARY;      PRT;   618 AA.
AC   Q96AA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC017356; AAH17356.1; -.
DR   PIR; S15590; S15590.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   618 AA;  67758 MW;  96DBD4C7C696E0A6 CRC64;

  Query Match             14.4%;  Score 389.5;  DB 4;  Length 618;
  Best Local Similarity   23.9%;  Pred. No. 2.5e-23;
  Matches  116;  Conservative   77;  Mismatches  167;  Indels  125;  Gaps   16;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |       || | ||  |    |   :|                       ||
Db        167 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 201

Qy         94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL-----------QGQSLTLT 142
               :::  |   :   :   :|         :   :| |::           :  | :
Db        202 SVLRGGKYAATSQVLLPSKD-----------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 250

Qy        143 LESPPGSSPSVQCR-------------------SPR---------GKNIQGGKTLSVSQL 174
               | ||  |  |  |                  |||         || :  | |    |
Db        251 AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA 310

Qy        175 ELQDSG--------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT 213
              | ::||                    :|| |  : : : |: :      |:  :  :
Db        311 EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR- 367

Qy        214 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                  ||  ||    :: :::: ::||:| |::  |  |  :|     |
Db        368 -----------VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH 414

Qy        274 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ 332
              |   |   |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     |
Db        415 TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD 474

Qy        333 VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG 387
              || |||:|::|   :   ::|||| || |:|: |:|   |||      | |: |: : : |
Db        475 VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG 534

Qy        388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD 447
               :| :| ||| :  |  |  ::| | |||| |  |:::: |      |    |:   :
Db        535 RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-----TEGEVSADEEGFE 589

Qy        448 GLWTT 452
                || |
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Db        590 NLWAT 594


RESULT 42
O77601
ID   O77601      PRELIMINARY;      PRT;    86 AA.
AC   O77601;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Lophocebus albigena albigena.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Lophocebus.
OX   NCBI_TaxID=75568;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057391; AAC25135.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20     >86      IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49      78      BY SIMILARITY.
FT   NON_TER      86      86
SQ   SEQUENCE   86 AA;  9463 MW;  2BD97A88464FE9AB CRC64;

  Query Match             14.4%;  Score 388;  DB 6;  Length 86;
  Best Local Similarity   87.1%;  Pred. No. 2e-24;
  Matches   74;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:|||||||||||||||:|||||||||||||:||||:|||||||||| |
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGTSPSVKCRSPRGKNIQVG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| |||||||||| |:||
Db         61 RTLSVPQLERQDSGTWTCTVSQDQK 85


RESULT 43
Q9BU10
ID   Q9BU10      PRELIMINARY;      PRT;   597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65274 MW;  2DAFA8FB7E055851 CRC64;

  Query Match             14.2%;  Score 385;  DB 4;  Length 597;
  Best Local Similarity   24.9%;  Pred. No. 5.6e-23;
  Matches  114;  Conservative   73;  Mismatches  164;  Indels  106;  Gaps   15;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |      || | ||  |   |  :|                          ||
Db        167 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 201

Qy         94 LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
               :::  |   :   :  :|      | |   |      | : ::     | :  | ||
Db        202 SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV 257

Qy        150 SPSVQCR-------------------SPR---------GKNIQGGKTLSVSQLELQDSG- 180
              |  |  |                   |||         || :  | |    | | ::||
Db        258 SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP 317

Qy        181 --------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL 220
                                 :|| |  : : : |: :      |:  :  :
Db        318 TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-------- 367

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
                ||  ||    :: :::: ::||:| |::  |  |  :|     |     |   |
Db        368 ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH 421

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS 339
              |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     | || |||:
Db        422 PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA 481

Qy        340 RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
              |::|  :   ::|||| || |:|: |:|   |||     | |: |: :  : | :| :|
Db        482 REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI 541

Qy        395 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||| :  |  |  ::| | |||| |  |:::  | |
Db        542 LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG 578


RESULT 44
Q9BQB8
ID   Q9BQB8      PRELIMINARY;      PRT;   597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle, and Lymph;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   EMBL; BC001872; AAH01872.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
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DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65300 MW;  2DAFAD50A6375851 CRC64;

  Query Match             14.2%;  Score 385;  DB 4;  Length 597;
  Best Local Similarity   24.9%;  Pred. No. 5.6e-23;
  Matches  114;  Conservative   73;  Mismatches  164;  Indels  106;  Gaps   15;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |       || | ||  |    |   :|                        ||
Db        167 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 201

Qy         94 LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
               :::  |   :   :   :|      | |   |      | : ::     | :  | ||
Db        202 SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV 257

Qy        150 SPSVQCR------------------SPR---------GKNIQGGKTLSVSQLELQDSG- 180
              |  |  |                  |||         || :  | |    | | ::||
Db        258 SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP 317

Qy        181 --------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL 220
                                  :|| |  : : : |: :       |:  :  :
Db        318 TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-------- 367

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
                 ||  ||    :: :::: ::||:| |::  |  |  :|      |      |   |
Db        368 ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH 421

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS 339
               |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     | || |||:
Db        422 PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA 481

Qy        340 RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
              |::|  :   ::|||| || |:|: |:|   |||     | |: |: :  : | :| :|
Db        482 REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI 541

Qy        395 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||  :  |  |  ::| | |||| |  |::::  | |
Db        542 LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG 578


RESULT 45
Q96BB9
ID   Q96BB9      PRELIMINARY;      PRT;   597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65039 MW;  4FCA3AD8ECE263D9 CRC64;

  Query Match             14.2%;  Score 385;  DB 4;  Length 597;
  Best Local Similarity   24.9%;  Pred. No. 5.6e-23;
  Matches  114;  Conservative   73;  Mismatches  164;  Indels  106;  Gaps   15;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |       || | ||  |    |   :|                        ||
Db        167 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 201

Qy         94 LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
               :::  |   :   :   :|      | |   |      | : ::     | :  | ||
Db        202 SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV 257

Qy        150 SPSVQCR------------------SPR---------GKNIQGGKTLSVSQLELQDSG- 180
              |  |  |                  |||         || :  | |    | | ::||
Db        258 SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP 317

Qy        181 --------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL 220
                                  :|| |  : : : |: :       |:  :  :
Db        318 TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-------- 367

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
                 ||  ||    :: :::: ::||:| |::  |  |  :|      |      |   |
Db        368 ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH 421

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS 339
               |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     | || |||:
Db        422 PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA 481

Qy        340 RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
              |::|  :   ::|||| || |:|: |:|   |||     | |: |: :  : | :| :|
Db        482 REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI 541

Qy        395 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |||  :  |  |  ::| | |||| |  |::::  | |
Db        542 LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG 578


RESULT 46
O77600
ID   O77600      PRELIMINARY;      PRT;   86 AA.
AC   O77600;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE   (Fragment).
OS   Lophocebus aterrimus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Lophocebus.
OX   NCBI_TaxID=75566;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC       SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC       ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR   EMBL; AF057390; AAC25134.1; -.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR007110; Ig-like.
KW   Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     19       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       20     >86      IG-LIKE C2-TYPE DOMAIN.
FT   CARBOHYD     79      79      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     49      78      BY SIMILARITY.
```

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FT   NON_TER      86     86
SQ   SEQUENCE   86 AA;  9476 MW;  A9D97A88464FE9BE CRC64;

  Query Match            14.2%;  Score 383;  DB 6;  Length 86;
  Best Local Similarity   85.9%;  Pred. No. 5.3e-24;
  Matches   73;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG 166
              |||||||:||||:|||||||||||||||:|||||||||||||:||||:|||||||||| |
Db          1 YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGTSPSVKCRSPRGKNIQVG 60

Qy        167 KTLSVSQLELQDSGTWTCTVLQNQK 191
              :|||| ||| |||||||| | |:||
Db         61 RTLSVPQLERQDSGTWTCNVSQDQK 85


RESULT 47
Q7TMT6
ID   Q7TMT6      PRELIMINARY;      PRT;   614 AA.
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053409; AAH53409.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   614 AA;  67746 MW;  839BAF3B8D124F89 CRC64;

  Query Match            14.1%;  Score 381;  DB 11;  Length 614;
  Best Local Similarity   23.3%;  Pred. No. 1.2e-22;
  Matches  139;  Conservative   77;  Mismatches  171;  Indels  210;  Gaps   25;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKN------SNQIKILGN----------QGSFLTKGP 73
              | | | :|:::| ||   :    | |         :: :|           | |  ||
Db         30 LVKPGASVKISCKAS-GYAFSSSWMNWVKQRPGKGLEWIGRVYPGDGDTNYNGKF--KGK 86

Qy         74 SKLN-DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH 132
              : |  |:: |   :          : :|  |||  | |   |      :   :|
Db         87 ATLTADKSSSTAYMQ--------LSSLTSEDSAVYFC-ARDYGSSYRFAYWG-------- 129

Qy        133 LLQGQSLTLTLESP--PGSSPSVQCRSP-RGKNI------------------------- 163
                 ||  :|:: ||   |   | | | ||   ||:
Db        130 --QGTLVTVSAESQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWNYQNNAE 187

Qy        164 ------------QGGKTLSVSQLELQDSGT-------WTCTVLQNQKKVEFKIDIVPCPA 204
                         ||| |: ||: |             | :   |  :     || ||
Db        188 VIQGIRTFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKIHYGGKNKDLH---VPIPA 244

Qy        205 --------------------PEPKS----CDKTHTCPELL--------------------- 220
                                 | |:      |: |:  |: :
Db        245 VAEMNPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPV 304

Qy        221 ------------------------------------------------GGPS----V 225
                                                             ||
Db        305 TIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILT 364

Qy        226 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 285
              |  ||   | : :|::  :||:| :::  :  :  :|     |    | |  |   | |:
Db        365 FTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTF 422

Qy        286 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLPPSR 340
                | :|  :|| | ||: | |::: ||:| :| |||    | |     | || |||:|
Db        423 SAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLPPAR 478

Qy        341 DELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLYSKL 395
              ::|  :   ::|||||||:|:|:|:|   ||  |:  | |: |: :  : | :| :| |
Db        479 EQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSIL 538

Qy        396 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
              || :  |  |  ::| | |||| :  |:::  |     |    |::   : ||||
Db        539 TVTEEEWNSGETYTCVVSHEALPHLVTERTVDKS-----TEGEVNAEEEGFENLWTT 590


RESULT 48
Q8WUX4
ID   Q8WUX4      PRELIMINARY;      PRT;   588 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   588 AA;  64438 MW;  FC60DBAD82B39FD7 CRC64;

  Query Match            14.1%;  Score 380;  DB 4;  Length 588;
  Best Local Similarity   24.8%;  Pred. No. 1.4e-22;
  Matches  113;  Conservative   73;  Mismatches  163;  Indels  106;  Gaps   15;

Qy         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
              :| : | |      || | ||  |   |  :|                          ||
Db        167 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------------------------FP 201

Qy         94 LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
              :::  |   :   :   :|      | |   |     | : ::     | :  | ||
Db        202 SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV 257
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Qy        150 SPSVQCR------------------SPR---------GKNIQGGKTLSVSQLELQDSG- 180
              |  |  |                  |||         || :  | |    | | ::||
Db        258 SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP 317

Qy        181 -------------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL 220
                              :|| |  : : : |: :       |:  :  :
Db        318 TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-------- 367

Qy        221 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
                 ||  ||    :: :::: ::||:| |::  |  |  :|      |      |   |
Db        368 ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH 421

Qy        281 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS 339
               |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     | || |||:
Db        422 PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA 481

Qy        340 RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
              |::|  :   ::|||| || |:|: |:|   |||     | |: |: :  :  | :| :|
Db        482 REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI 541

Qy        395 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
              ||| :  |  |  ::| | |||| |  |:::  |
Db        542 LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS 576


RESULT 49
Q8VCX7
ID   Q8VCX7      PRELIMINARY;      PRT;   613 AA.
AC   Q8VCX7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018315; AAH18315.1; -.
DR   MGD; MGI:96448; Igh-6.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67855 MW;  41A9384DD4C22862 CRC64;

  Query Match             13.8%;  Score 373.5;  DB 11;  Length 613;
  Best Local Similarity   25.2%;  Pred. No. 5.1e-22;
  Matches  121;  Conservative   87;  Mismatches  157;  Indels  115;  Gaps   23;

Qy         37 VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF-- 92
              | : | |      :| | |   |  :::    :| |               |   | :
Db        161 VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT--------------LRTGGKYLA 205

Qy         93 ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE 144
                   |:    :| || | :|::          :|   | | |:    :   :  : :
Db        206 TSQVLLSPKSILEGSDEYLVCKIH----------YG-GKNRDLHVPIPAVAEMNPNVNVF 254

Qy        145 SPP-----GSSP---SVQCR----SPR---------GKNIQGG---------------- 166
               ||     | :|    : |     :|:         || :: |
Db        255 VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT 314

Qy        167 ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG 222
                  ||::|:::  :   :|| |  : : : |  ::    |  | :        ::|
Db        315 YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST--------DIL-- 362

Qy        223 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 282
                 |  ||    | : :|::  :||:| ::::  :  :  :|      |    | |  |   |
Db        363 --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN 418

Qy        283 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP 337
               |:    | :|  :|| | ||: | |::: ||:|  :| |||    | |     | || ||
Db        419 GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP 474

Qy        338 PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY 392
              |:|::|  :   ::||||||| |:||:|:|   ||  |:  | |: |: :  : | :| :
Db        475 PAREQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH 534

Qy        393 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
              | ||| :  |  |  ::| | |||| :  |:::: |      |    |::   : ||||
Db        535 SILTVTEEEWNSGETYTCVVGHEALPHLVTERTVDKS-----TEGEVNAEEEGFENLWTT 589


RESULT 50
Q86TT1
ID   Q86TT1      PRELIMINARY;      PRT;   375 AA.
AC   Q86TT1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Human full-length cDNA clone CS0DD006YL02 of neuroblastoma of Homo
DE   sapiens (Human).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Neuroblastoma;
RA   Genoscope;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Neuroblastoma;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RT   "Full-length cDNA libraries and normalization.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX161420; CAD61894.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Plasmid.
SQ   SEQUENCE   375 AA;  41272 MW;  7ACD1AF4399C5EFE CRC64;

  Query Match             13.6%;  Score 366.5;  DB 4;  Length 375;
  Best Local Similarity   28.6%;  Pred. No. 9.6e-22;
  Matches   98;  Conservative   59;  Mismatches  125;  Indels   61;  Gaps   12;

Qy        139 LTLTLESPPGSSPSVQCR------------------SPR---------GKNIQGGKTLS 170
              | :  | ||  |  |  |                  |||         || :  | |
Db         25 LPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTD 84

Qy        171 VSQLELQDSG------TWTCTVLQ----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL 220
              | | ::||       | | |: :     :|      ::|        :  |          :
Db         85 QVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASS---------M 135

Qy        221 GGPS------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 274
              ||        ||  ||     :: :::: ::||:| |::  |  |  :|     |     |
Db        136 CGPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHT 193

Qy        275 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV 333
                   |:|:  |   ::   || :|: : | |::  ||:|:::|||: ||     | |
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```
Db        194 NISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDV 253

Qy        334 YTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGS 388
              | |||:|::|  :   ::|||| || |:|: |:|   |||     | |: |: :  : |
Db        254 YLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGR 313

Qy        389 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              :| :| ||| :  |  |  ::| | |||| |  |::::  | |
Db        314 YFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG 356


RESULT 51
Q13969
ID   Q13969      PRELIMINARY;      PRT;    71 AA.
AC   Q13969;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4 protein (Fragment).
GN   CD4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zverev V.V., Blinov V.M., Nedospasov S.A.;
RT   "Splice-mediated insertion of antisence and sence Alu repeats in human
RT   CD4 gene: identification of three exons of CD4 mRNA.";
RL   Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95407135; PubMed=7676667;
RA   Zverev V.V., Sidorov A.V., Nedospasov S.A., Maliushova V.V.,
RA   Udalova I.A., Andzhaparizde O.G., Blinov V.M.;
RT   "[Nucleotide sequence of two exons of the human T-lymphocyte CD4
RT   receptor gene].";
RL   Vopr. Virusol. 40:100-102(1995).
DR   EMBL; X87579; CAA60883.1; -.
DR   EMBL; S79267; AAB35273.1; -.
DR   PIR; I60082; I60082.
DR   HSSP; P01730; 1CDY.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
FT   NON_TER      71     71
SQ   SEQUENCE   71 AA;  7844 MW;  A5C9D84816135C86 CRC64;

  Query Match             13.2%;  Score 357;  DB 4;  Length 71;
  Best Local Similarity   98.6%;  Pred. No. 5.6e-22;
  Matches   70;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTK 71
              ||||||||||||
Db         61 ILGNQGSFLTK 71


RESULT 52
Q7T0R1
ID   Q7T0R1      PRELIMINARY;      PRT;   587 AA.
AC   Q7T0R1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056078; AAH56078.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   587 AA;  64933 MW;  646B5FD0FA414E8D CRC64;

  Query Match             12.8%;  Score 345.5;  DB 13;  Length 587;
  Best Local Similarity   25.8%;  Pred. No. 9.7e-20;
  Matches  119;  Conservative   77;  Mismatches  189;  Indels   77;  Gaps   18;

Qy         31 GKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSF----LTKGPSKLNDRADSRR 84
              |:  | | : | |    ::| | | : |          |:     : |    : : :
Db        149 GESMDPVTIGCLAKDFLPETISFTWGDKNNASYSTGLKSYKPVMQSSGTYSASSQVNVAS 208

Qy         85 SLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ----------------------LLV 122
              ::||  |      | |  |:   |  || :|: |:                      | :
Db        209 AVWD--NIEQFYCNAKHLDT---IKSVELKKDPVKPVEKPVVSIHPPSKDALALNESLFI 263

Qy        123 FGLTAN-SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---RGKNIQGGKTLSVSQLELQD 178
                |  | : ||:     :   |::   ::  |:   |   : :  :    ||::: |
Db        264 VCLATNFTPTHI-----VIKWLKNGNQTTEGVRVEEPVEDKKRGYEATSYLSITRKEWDL 318

Qy        179 SGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS--VFLFPPKPKDTL 236
              ::| |              :     : : |:  |:  |   :   |  |   ||   :::
Db        319 DTLYSCVV-----------EHAESGSLQEKNMSKSLMCDTPITPTSIQVITIPPS-LESI 366

Qy        237 MISRTPEVTCVVVDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNS--TYRVVSVLTV 293
              ::  :||:| :::: :     :|:   | :    ||:  :  ||   || |    ||
Db        367 FEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTV 426

Qy        294 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTC 352
              :| | | : ||| :  | :  |  : | ||:   | ||  ||  :||:| :  :|||
Db        427 CADEWNNDK-FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTC 485

Qy        353 LVKGFYPSDIAVEW--ESNGQPENNYKTTP------PVLDSDGSFFLYSKLTVDKSRWQQ 404
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Db        486 LVKGFSPSEIFVKWLHKNEAVPKQNYINTSINDELLPKGQKSGKFFLYSLHTIDIKDWDA 545

Qy        405 GNVFSCSVMHEALHNHYTQKSLSLSPG--------LQLDETC 438
Db        546 GDSFSCVVGHESLPLQLTQRSIDKSSGKPTNVNVSLVLSDTC 587


RESULT 53
Q7Z379
ID   Q7Z379      PRELIMINARY;      PRT;   478 AA.
AC   Q7Z379;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686K04218 (Fragment).
GN   DKFZP686K04218.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538066; CAD97996.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   478 AA;  51620 MW;  4AFCB541F3217CA1 CRC64;

  Query Match             12.4%;  Score 336;  DB 4;  Length 478;
  Best Local Similarity   27.1%;  Pred. No. 4.4e-19;
  Matches  135;  Conservative   65;  Mismatches  210;  Indels   88;  Gaps   24;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTASQKK--SIQFHWKNSNQI 59
Db          1 KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQA 60

Qy         60 KILGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYIC----- 109
Db         61 PGRGLEWMGYIYYSGSTYYNPSLESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVG 120

Qy        110 -----EVEDQKEEVQL--------LVFGLTANSDTH--------LLQG----QSLTLTLE 144
Db        121 LGTAFDIWGQGTVVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWS 180

Qy        145 SPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLEL-----QDSGTWTCTVLQNQKKVEFKID 198
Db        181 E---SGQNVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---D 234

Qy        199 I-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 257
Db        235 VTVPCPVPPPPPC-----C-----HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASG 282

Qy        258 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 317
Db        283 ATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPL 340

Qy        318 EKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PEN 374
Db        341 TANITKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPRE 399

Qy        375 NYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        400 KYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVSHEALPLAFTQKTIDRLAG 459

Qy        432 -----------LQLDETC 438
Db        460 KPTHVNVSVVMAEVDGTC 477


RESULT 54
Q7Z374
ID   Q7Z374      PRELIMINARY;      PRT;   492 AA.
AC   Q7Z374;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686C02218 (Fragment).
GN   DKFZP686C02218.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX538077; CAD98001.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   492 AA;  53776 MW;  1E7A15760F0CA74B CRC64;

  Query Match             11.9%;  Score 322.5;  DB 4;  Length 492;
  Best Local Similarity   26.3%;  Pred. No. 5.9e-18;
  Matches  131;  Conservative   68;  Mismatches  211;  Indels   89;  Gaps   23;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSN 57
Db         14 KHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQP 73

Qy         58 QIKILGNQGSFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYIC--EVE 112
Db         74 PGKGLEWIGSIYYNENTYYSPSLKSRLTIFVDTSKNHFSLRLTSVTAADTAVYYCVRHVE 133

Qy        113 ----------------DQKEEVQLLVFGLTANSDTH--------LLQG----QSLTLTL 143
Db        134 GPYGWFDPWGQGTLVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTW 193

Qy        144 ESPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLEL-----QDSGTWTCTVLQNQKKVEFKI 197
Db        194 SE---SGQNVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ--- 247

Qy        198 DI-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 256
Db        248 DVTVPCPVPPPPPC-----C-----HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDAS 295

Qy        257 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 316
Db        296 GATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWTHGETFTCTAAHPELKTP 353

Qy        317 IEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PE 373
Db        354 LTANITKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPR 412

Qy        374 NNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 430
Db        413 EKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLA 472

Qy        431 G-----------LQLDETC 438
Db        473 GKPTHVNVSVVMAEVDGTC 491


RESULT 55
Q99LA6
ID   Q99LA6      PRELIMINARY;      PRT;   484 AA.
AC   Q99LA6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
```

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003495; AAH03495.1; -.
DR   PIR; F33932; F33932.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   484 AA;  52567 MW;  8EAEA4F9BCF582FA CRC64;

  Query Match             11.7%;  Score 315.5;  DB 11;  Length 484;
  Best Local Similarity   26.3%;  Pred. No. 2.2e-17;
  Matches  128;  Conservative   67;  Mismatches  200;  Indels   91;  Gaps   20;

Qy         13 VLQLALLPAATQGNKV---------VLGKKGDTVELTCTASQKKSIQF--HWKNSNQIKI 61
Db          4 VWTLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKG 63

Qy         62 LGNQGSF-LTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEE 117
Db         64 LKWMGWVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDYDYD 123

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLES-----------PPGSS--------------PS 152
Db        124 IYAM---------DYWGQGTSVTVSSESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPS 174

Qy        153 VQCRSPRGKN-------------IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVE 194
Db        175 GTMNVTWGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ 234

Qy        195 FKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 254
Db        235 -ELD-VNCSGPTPPPPITIPSCQ-----PSLSLQRPALED-LLLGSDASITCTLNGLRNP 286

Qy        255 DPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 311
Db        287 EGAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP 340

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG 370
Db        341 E-SGTLTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGN 399

Qy        371 Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
Db        400 EELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKT 459

Qy        426 LSLSPG 431
Db        460 IDRLSG 465


RESULT 56
Q99KA4
ID   Q99KA4      PRELIMINARY;      PRT;   487 AA.
AC   Q99KA4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004786; AAH04786.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   487 AA;  52554 MW;  7DC8E96DB333077B CRC64;

  Query Match             11.6%;  Score 314.5;  DB 11;  Length 487;
  Best Local Similarity   26.2%;  Pred. No. 2.7e-17;
  Matches  132;  Conservative   76;  Mismatches  188;  Indels  107;  Gaps   25;

Qy          1 MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW-- 53
Db          1 MNFGLSLIFLVLVLKGVQCEVQLVESGGGLV---KPGGSLKLSCAASGFTFSSYAMSWVR 57

Qy         54 ----KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC 109
Db         58 QTPEKRLEWVATISDGGSY-TYYPDNVKGRFTISRDN-AKNNLYLQMSHLKSEDTAMYYC 115

Qy        110 EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-QCRSPR--------- 159
Db        116 -----ARDMGGSPYGGYSRFD---YWGQGTTITVSSESARNPTIYPLTLPRALSSDPVII 167

Qy        160 --------------------GKNIQ-----------GGKTLSVSQL-----ELQDSGTWT 183
Db        168 GCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTLPAVECPEGESVK 226

Qy        184 CTVLQNQKKVEFKIDI------VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM 237
Db        227 CSVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH----------PSLSLQRPALED-LL 272

Qy        238 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVL 294
Db        273 LGSDASLTCTLNGLRNPEGAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGC 326

Qy        295 HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCL 353
Db        327 AERWNSGASFKCTVTHPESDT-LTGTIAKITVNTFPPQVHLLPPPSEELALNELVSLTCL 385

Qy        354 VKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVF 408
Db        386 VRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQY 445

Qy        409 SCSVMHEALHNHYTQKSLSLSPG 431
Db        446 SCMVGHEALPMNFTQKTIDRLSG 468


RESULT 57
Q8VCX4
ID   Q8VCX4      PRELIMINARY;      PRT;   489 AA.
AC   Q8VCX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-VJ558 OR AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018322; AAH18322.1; -.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   489 AA;  53208 MW;  CC85B1194DAFEF2C CRC64;

  Query Match             11.6%;  Score 313.5;  DB 11;  Length 489;
  Best Local Similarity   24.9%;  Pred. No. 3.2e-17;
  Matches  118;  Conservative   70;  Mismatches  181;  Indels  105;  Gaps   24;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HW---KNSNQIKILG--NQGSFLTKGPSKLNDRADS 82
              | | | :|:|:| ||      :  ||   ::   :: :|  | ||    |  | |::
Db         30 LVKPGASVKLSCKASGYTFSDYFIHWIKQRSGQGLEWIGWFNPGS----GSIKFNEKFKD 85

Qy         83 RRSLWDQGNFPLI---IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL----LQ 135
              : :|    :   :   :  | |||  | |   : :            | |  |
Db         86 KATLTADKSSTTVYMDLSRLTSEDSAVYFCARHEDR----------GNYDGSLAWFVYW 134

Qy        136 GQSLTLTLESPPGSSPSV------QCRS-------------PRG-KNI---QGGKTLSV 171
              ||   :|: : |   |::      |  |               | |  |:   : || ::
Db        135 GQGTLVTVSAEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITT 194

Qy        172 SQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH----------TCPEL 219
                 |  | :| :        :  :  | ||  |   |   |              || :
Db        195 VNFPPALASGGRYTMS-------SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGI 247

Qy        220 LGGPSVFLFPPKPK-----------DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDG 266
                |:    || |               : |::     :|| :  :   |||   | |
Db        248 CSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW---- 298

Qy        267 VEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
               |    |   :::   ::   | | |||    : | :|  :|| |::      :  ||:|
Db        299 -EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAK 356

Qy        324 AKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTT 379
                  |||: |||  :||  |: |||||||: | | :: | |    :   ||:
Db        357 VTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFE 416

Qy        380 PPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
               |     :|  :: : | | |    |:||: :|| | ||||  ::|||::    |
Db        417 PLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 470


RESULT 58
Q9NPP6
ID   Q9NPP6      PRELIMINARY;      PRT;   416 AA.
AC   Q9NPP6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin heavy chain variant (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
RA   Lehrach H., Poustka A., Lundeberg J.;
RT   "The European IMAGE consortium for integrated Molecular analysis of
RT   human gene transcripts.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL389978; CAB97534.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   416 AA;  44786 MW;  8C41708BB8AB4687 CRC64;

  Query Match             11.5%;  Score 312;  DB 4;  Length 416;
  Best Local Similarity   27.8%;  Pred. No. 3.4e-17;
  Matches  116;  Conservative   61;  Mismatches  163;  Indels   78;  Gaps   21;

Qy         78 DRADSRRSLWD------QGNFPLIIKNLKIEDSDTYIC-------EVEDQKEEVQL---- 120
              | ||| :  :        : :  | : :|::||:  | |        :|  |   | :
Db         19 DYADSVKGRFTVSRDTAKNSLSLQMSSLRVEDTAVYYCARTYYGMDVWGQGTTVTVSSAS 78

Qy        121 ----LVFGLTANSDTH--------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNI 163
                  || |: :|             |:||    : |::|      |  :|  |: |  ::
Db         79 PTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDA 135

Qy        164 QGGKTLSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCP 217
                |    : ||| |       |  : || |        :   |: |||| | |  |     |
Db        136 SGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPC-----C- 186

Qy        218 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 277
                  | :  |  |  :| |::     :|| :  :  :      | |      :  :|   |
Db        187 ----HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPP 238

Qy        278 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 337
              |      | | |||    | | :|: : |  ::   |  |:   |:|: |    |:|: ||
Db        239 ERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLP 297

Qy        338 PSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFL 391
              |  :||  |: |:|||| :|| | |: | |    |  |   | |     : | |  :| :
Db        298 PPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAV 357

Qy        392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----------LQLDETC 438
              | | |    |::|: ||| | ||||   :|||::    |            ::| ||
Db        358 TSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC 415


RESULT 59
Q91WT1
ID   Q91WT1      PRELIMINARY;      PRT;   481 AA.
AC   Q91WT1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013490; AAH13490.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
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SQ   SEQUENCE   481 AA;  52105 MW;  97DF68D159463F65 CRC64;

  Query Match             11.5%;  Score 311;  DB 11;  Length 481;
  Best Local Similarity   24.7%;  Pred. No. 5.1e-17;
  Matches  120;  Conservative   67;  Mismatches  187;  Indels  112;  Gaps   23;

Qy         15 QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG------ 66
              |: || :  :     | | | :|:::| ||     |   ||     :|    ||
Db         20 QVQLLQSGPE-----LVKPGASVKISCKASGYTFTSYYIHW-----VKQRPGQGLVWIGW 69

Qy         67 SFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF 123
               :   | :| |::   : :|       : : :|  |||  | |
Db         70 IYPGDGNTKYNEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFC-------------- 115

Qy        124 GLTANSDTHLLQGQSLTLTLESPPGSSPSV------QCRS--------------PRG-KN 162
                        ||  |||: | |   |::       |  |              | |  |
Db        116 -TRGGGWAFDYWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMN 174

Qy        163 I---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH--- 214
              :   : || ::       |   | :| :         :  :  | || |   |   |
Db        175 VTWGKSGKDITTVNFPPALASGGRYTMS-------SQLTLPAVECPEGESVKCSVQHDSN 227

Qy        215 -------TCPELLGGPSVFLFPPKPK-----------DTLMISRTPEVTCVVVDVSHED 255
                    || :   |:    | | |             : |::     :|| :  :   |
Db        228 PVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RD 282

Qy        256 PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||   | |      |    |   :::   ::   | | |||    : | :|  :|| |::
Db        283 PEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP 337

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG 370
                : ||:|       |||: |||  :||  |: |||||||: | | :: | |
Db        338 ESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN 396

Qy        371 Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              :   ||:      |    :|  :: : | | |    |:||: :|| | |||| ::|||:
Db        397 EELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKT 456

Qy        426 LSLSPG 431
              :   |
Db        457 IDRLSG 462


RESULT 60
Q8K172
ID   Q8K172      PRELIMINARY;      PRT;   482 AA.
AC   Q8K172;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to expressed sequence AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028249; AAH28249.1; -.
DR   PIR; F33932; F33932.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
SQ   SEQUENCE   482 AA;  52121 MW;  A06FF083E771D084 CRC64;

  Query Match             11.5%;  Score 311;  DB 11;  Length 482;
  Best Local Similarity   25.0%;  Pred. No. 5.1e-17;
  Matches  117;  Conservative   68;  Mismatches  183;  Indels  100;  Gaps   22;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW---KNSNQIKILGNQGSFLTKGPSKLNDRADSRR 84
              | | | :|:|:| ||     |   ||    :    :: :|        | :| |::  |:
Db         30 LVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDP--NSGGTKYNEKFKSKA 87

Qy         85 SLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL 141
              :|        : : :|  |||  | |  |                 : |      ||  ::
Db         88 TLTVDKPSSTAYMQLSSLTSEDSAVYYCTRE-------------GDYDAMDYWGQGTSV 133

Qy        142 TLESPPGSSPSV------QCRS--------------PRG-KNI---QGGKTLSVSQL--E 175
              |: | |   |::      |  |              | |  |:   : || ::
Db        134 TVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPA 193

Qy        176 LQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH----------TCPELLGGPSV 225
              |   | :| :         :  :  | ||  |   |   |           || :   |:
Db        194 LASGGRYTMS-------SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGICSPPTT 246

Qy        226 FLFPPKPK-----------DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNA 272
                 || |             : |::     :|| :  :   |||   | |     |
Db        247 ---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTG 296

Qy        273 KTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
              |   :::   ::   | | |||    : | :|  :|| |::       :  ||:|
Db        297 KDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTF 355

Qy        330 EPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDS 385
               |||: |||  :||  |: |||||||: | | :: | |    :   ||:      |
Db        356 PPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPG 415

Qy        386 DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              :|  :: : | | |    |:||: :|| | |||| ::|||::    |
Db        416 EGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 463


RESULT 61
Q91X92
ID   Q91X92      PRELIMINARY;      PRT;   482 AA.
AC   Q91X92;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011181; AAH11181.1; -.
DR   PIR; F33932; F33932.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   482 AA;  51865 MW;  312E01F9C1BC7F3C CRC64;

  Query Match             11.4%;  Score 307;  DB 11;  Length 482;
  Best Local Similarity   25.0%;  Pred. No. 1.1e-16;
  Matches  123;  Conservative   69;  Mismatches  198;  Indels  102;  Gaps   24;

Qy         10 LLLVLQLALLPAATQGNKVVLGKKG-------DTVELTCTAS--QKKSIQFHWKNSNQIK 60
Db          4 LALLLCLVTFPSCAL-SQVQLKESGPDLVAPSQSLSITCTVSGFALTSYAISWVRQPPGK 62

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIKNLKIEDSDT--YICEVEDQKEE 117
Db         63 GLEWLGVIWTGGVTNYNSALKSRLSISKDNSKSQVFLKMNSLQTNDTARYYC-ARDSNYE 121

Qy        118 VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV------QCRS-------------- 157
Db        122 GAMDYW------------GQGTSVTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYF 169

Qy        158 PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211
Db        170 PSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-------SQLTLPAVECPEGESVKCS 222

Qy        212 KTH----------TCPELLGGPSVFLFPPKPK-----------DTLMISRTPEVTCVVV 249
Db        223 VQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLN 279

Qy        250 DVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYK 305
Db        280 GL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFK 332

Qy        306 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAV 364
Db        333 CTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLV 391

Qy        365 EWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 419
Db        392 RWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPM 451

Qy        420 HYTQKSLSLSPG 431
Db        452 NFTQKTIDRLSG 463


RESULT 62
Q29027
ID   Q29027      PRELIMINARY;      PRT;    99 AA.
AC   Q29027;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4, allele 1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=#1183; TISSUE=Blood;
RX   MEDLINE=93329116; PubMed=8335933;
RA   Gustafsson K., Germana S., Sundt T.M., Sachs D.H., LeGuern C.;
RT   "Extensive allelic polymorphion in an exposed region of the
RT   miniature. . . . . .";
RL   J. Immunol. 151:1365-1370(1993).
DR   EMBL; X65629; CAA46583.1; -.
DR   PIR; I47131; S21461.
DR   HSSP; P01730; 1CDY.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  11170 MW;  40BF080699CF5D0C CRC64;

  Query Match             11.3%;  Score 305.5;  DB 6;  Length 99;
  Best Local Similarity   60.2%;  Pred. No. 1.5e-17;
  Matches   59;  Conservative   16;  Mismatches   22;  Indels    1;  Gaps    1;

Qy         32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRSLWDQG 90
Db          1 KAGDLAELPCHSSQKKNLPFNWKNSNQTKILGGHGSFWHTASVTELTSRLDSKKNMWDHG 60

Qy         91 NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN 128
Db         61 SFPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS 98


RESULT 63
Q91Z07
ID   Q91Z07      PRELIMINARY;      PRT;   486 AA.
AC   Q91Z07;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010324; AAH10324.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   486 AA;  52682 MW;  4FEF835125DA870B CRC64;

  Query Match             11.3%;  Score 305;  DB 11;  Length 486;
  Best Local Similarity   25.7%;  Pred. No. 1.6e-16;
  Matches  129;  Conservative   79;  Mismatches  188;  Indels  106;  Gaps   25;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLG----KKGDTVELTCTAS--QKKSIQFHWK 54
Db          1 MNFGL----RLIFLVLALKGVQCEVHLVESGGGLVKPGGSLKLSCVVSGFSFTSYDMSWV 56

Qy         55 NSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIK--NLKIEDSDTYICEV 111
Db         57 RQTPERRLEWVAAITSGGNTYYPDNVKGRFTVSRDNAKYTLYLQMSSLKSEDTAMYYC-- 114

Qy        112 EDQKEEVQLLVF-GLTANSDTHLLQGQSLTLTLESPPGSSPSV-QCRSPR---------- 159
Db        115 --VRPEIPIYYYSGSYFDS-----WGQGTTITVSSESARNPTIYPLTLPRALSSDPVIIG 167

Qy        160 ------------------GKNIQ----------GGKTLSVSQL-----ELQDSGTWTC 184
Db        168 CLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTLPAVECPEGESVKC 226

Qy        185 TVLQNQKKVEFKIDI------VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMI 238
Db        227 SVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH----------PSLSLQRPALED-LLL 272
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Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLH 295
Db        273 GSDASLTCTLNGLRNPEGAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCA 326

Qy        296 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLV 354
Db        327 ERWNSGASFKCTVTHPESDT-LTGTIAKITVNTFPPQVHLLPPPSEELALNELVSLTCLV 385

Qy        355 KGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFS 409
Db        386 RAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQYS 445

Qy        410 CSVMHEALHNHYTQKSLSLSPG 431
Db        446 CMVGHEALPMNFTQKTIDRLSG 467


RESULT 64
Q8K0F2
ID   Q8K0F2      PRELIMINARY;      PRT;   488 AA.
AC   Q8K0F2;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to expressed sequence AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC031703; AAH31703.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
SQ   SEQUENCE   488 AA;  53127 MW;  0E3B156E155733F0 CRC64;

  Query Match             11.3%;  Score 304;  DB 11;  Length 488;
  Best Local Similarity   24.2%;  Pred. No. 2e-16;
  Matches  121;  Conservative   73;  Mismatches  188;  Indels  118;  Gaps   24;

Qy         14 LQLALLPAATQGNKVV--------LGKKGDTVELTCTAS--QKKSIQFHW---KNSNQIK 60
Db          6 IMLFLAAAATGVHSQVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLE 65

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYIC-------- 109
Db         66 WIGRIDP--NSGDTKFNEKFRTKATLTVDKPSSTVYMHLRSLTSEDSAVYYCTRRGLFYS 123

Qy        110 EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV------QCRS------ 157
Db        124 DYVDYSMD---------------YWGQGTSVTVSSEPAREPTIYPLTFPQALSSDPVII 167

Qy        158 --------PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCP 203
Db        168 GCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-------SQLTLPAVECP 220

Qy        204 APEPKSCDKTH----------TCPELLGGPSVFLFPPKPK-----------DTLMISRT 241
Db        221 EGESVKCSVQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSD 277

Qy        242 PEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQD 297
Db        278 ASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAER 330

Qy        298 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKG 356
Db        331 WNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRA 389

Qy        357 FYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCS 411
Db        390 FNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCM 449

Qy        412 VMHEALHNHYTQKSLSLSPG 431
Db        450 VGHEALPMNFTQKTIDRLSG 469


RESULT 65
Q90544
ID   Q90544      PRELIMINARY;      PRT;   684 AA.
AC   Q90544;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Novel antigen receptor precursor.
OS   Ginglymostoma cirratum (Nurse shark).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC   Ginglymostomatidae; Ginglymostoma.
OX   NCBI_TaxID=7801;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=95183140; PubMed=7877689;
RA   Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA   Flajnik M.F.;
RT   "A new antigen receptor gene family that undergoes rearrangement and
RT   extensive somatic diversification in sharks.";
RL   Nature 374:168-173(1995).
DR   EMBL; U18701; AAB48195.1; -.
DR   PIR; S60266; S60266.
DR   HSSP; P01842; 2MCG.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 6.
DR   SMART; SM00407; IGc1; 4.
DR   PROSITE; PS50835; IG_LIKE; 6.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Receptor; Signal.
FT   SIGNAL       1     18       POTENTIAL.
FT   CHAIN       19    684       NOVEL ANTIGEN RECEPTOR.
SQ   SEQUENCE   684 AA;  75224 MW;  2FF9D2071CDA6DFD CRC64;

  Query Match             11.2%;  Score 301.5;  DB 13;  Length 684;
  Best Local Similarity   25.1%;  Pred. No. 5.1e-16;
  Matches  107;  Conservative   66;  Mismatches  161;  Indels   92;  Gaps   16;

Qy         37 VELTCTASQKKSIQFHWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLWDQGNFPL 94
Db        321 VEYTCSAKQDQSSTPVVKRTRKARVEPTKPHLRLLPPSPEEIQSTSSATLTCLIRGFYPD 380

Qy         95 IIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ 154
Db        381 KV------------SVSWQKDDVS--VSANVTNFPTAL--EQDLTFSTRS--------- 414

Qy        155 CRSPRGKNIQGGKTLSVSQLELQDSGTWTCT------------VLQNQKKVEFKIDIVPC 202
Db        415 ------------LLNLTAVEWKSGAKYTCTASHPPSQSTVKRVIRNQ-----KVD---- 452

Qy        203 PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFN 261
Db        453 -------CRQTDI--------SVSLLKP-PFEEIWTQQTATIVCEIV---YSDLENIKVF 493
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Qy        262 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 321
Db        494 WQVNGVERKKGVETQNPEWSGSKSTIVSKLKVMASEWDSGTEYVCLVEDSELPTPVKASI 553

Qy        322 SKAK-GQPREPQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKT 378
Db        554 RKANVSQMHPPKVYLLHPSTDEIDTENSATLMCLATNFHPAEIYVGWMANDTLLDSGYRT 613

Qy        379 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH-------NHYTQKSLSLSPG 431
Db        614 QVDSEKGSGSSFVTDRLRLTAAEWNSDTTYSCLVGHPSLNRDLIRSTNKSNGKPSSVNVS 673

Qy        432 LQLDET 437
Db        674 VVLSDT 679


RESULT 66
Q91XE1
ID   Q91XE1      PRELIMINARY;      PRT;   480 AA.
AC   Q91XE1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010798; AAH10798.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   480 AA;  51936 MW;  20B9234EEF2B41ED CRC64;

  Query Match             11.1%;  Score 300.5;  DB 11;  Length 480;
  Best Local Similarity   24.2%;  Pred. No. 3.7e-16;
  Matches  121;  Conservative   69;  Mismatches  200;  Indels  111;  Gaps   23;

Qy          2 NRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----------QKKS 48
Db          1 NFGLSLIFLVLILKGVLCDVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPE 60

Qy         49 IQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYI 108
Db         61 KRLEW-----VATISNSG-YATHYPDSMKGRFTISRDN-AQNTVLLQMTSLNSEDTAVYY 113

Qy        109 CEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV------QCRS----- 157
Db        114 CTRGD------YWYFD---------VWGAGTTVTVSSEPAREPTIYPLTFPQALSSDPVI 158

Qy        158 ---------PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPC 202
Db        159 IGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-------SQLTLPAVEC 211

Qy        203 PAPEPKSCDKTH----------TCPELLGGPSVFLFPPKPK-----------DTLMISR 240
Db        212 PEGESVKCSVQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGS 268

Qy        241 TPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQ 296
Db        269 DASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAE 321

Qy        297 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVK 355
Db        322 RWNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVR 380

Qy        356 GFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSC 410
Db        381 AFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSC 440

Qy        411 SVMHEALHNHYTQKSLSLSPG 431
Db        441 MVGHEALPMNFTQKTIDRLSG 461


RESULT 67
Q96K68
ID   Q96K68      PRELIMINARY;      PRT;   494 AA.
AC   Q96K68;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ14473.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mammary gland;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027379; BAB55072.1; -.
DR   PIR; S21205; S21205.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   494 AA;  53088 MW;  9A1D7AEB5AEE4C0E CRC64;

  Query Match             11.1%;  Score 300.5;  DB 4;  Length 494;
  Best Local Similarity   25.3%;  Pred. No. 3.9e-16;
  Matches  123;  Conservative   71;  Mismatches  193;  Indels   99;  Gaps   24;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKILGNQGSFL-----TKGPSKL 76
Db         30 LVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYYRDSVKGRFTI 89

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
Db         90 S-RDNAKNSLYLQMN------SLRVDDTAVYYCARDSCNGAI---CYGFSP-------WG 132

Qy        137 QSLTLTLESPPGSSPSV----QCRSPRGKN------IQG---GKTLSVSQLE-------- 175
Db        133 QGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTAR 192

Qy        176 ----LQDSG----------TWTCTVLQNQKKVEFKI--------DI-VPCPAPEPKSCDK 212
Db        193 NFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPS 252

Qy        213 THTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269
Db        253 PSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK- 309
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Qy        270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
              :|   | |       | | |||    : | :|| : |  :       |:  |:||: |
Db        310 -SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTF 367

Qy        330 EPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-S 385
              |:|: |||  :||  |: |:|||| :|| | |: | |    |  |   | |     : |
Db        368 RPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPS 427

Qy        386 DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG----------L 432
              |  :| : | | |    |::|: ||| | ||||   :|||::    |
Db        428 QGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMA 487

Qy        433 QLDETC 438
              ::| ||
Db        488 EVDGTC 493


RESULT 68
Q91WT3
ID   Q91WT3      PRELIMINARY;      PRT;   481 AA.
AC   Q91WT3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-VJ558 OR AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013488; AAH13488.1; -.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   481 AA;  52022 MW;  4EEB5C253038B718 CRC64;

  Query Match           11.0%;  Score 298.5;  DB 11;  Length 481;
  Best Local Similarity   24.3%;  Pred. No. 5.5e-16;
  Matches  121;  Conservative   69;  Mismatches  183;  Indels  125;  Gaps   24;

Qy         16 LALLPAATQGNKVV--------LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG- 66
              | |:  ||  |  |        : : | :|:|:|  |   :   :|   | :|    ||
Db          8 LFLVATATGVNSQVQLQQPGAEIVRPGASVKLSCKTS-GYTFTDYW--MNWVKQRPGQGL 64

Qy         67 ----------SFLT-----KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV 111
                        |: :     || :   | : |        :  ::: :|  |||  | |
Db         65 EWIGAIDPFDSYTSYNQKFKGTTLTVDTSSS--------SAYMLLSSLTSEDSAVYFC-- 114

Qy        112 EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV------QCRS-------- 157
                          :    ||  |||: | |   |::      | |
Db        115 ------------ARGPRDSSGYYWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGC 162

Qy        158 ------PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAP 205
                  | |  |:   : || ::       |   | :| :       :  :  | ||
Db        163 LIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-------SQLTLPAVECPEG 215

Qy        206 EPKSCDKTH----------TCPELLGGPSVFLFPPKPK-----------DTLMISRTPE 243
              |   |  |          || :   |:    || |           : |::
Db        216 ESVKCSVQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDAS 272

Qy        244 VTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWL 299
              :|| :  :   |||   | |     |    |  :::   ::   | | |||    : |
Db        273 ITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWN 325

Qy        300 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFY 358
              :|  :|| |::      :  ||:|       |||: |||  :||  |: |||||: |
Db        326 SGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFN 384

Qy        359 PSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVM 413
              | :: | |    :   ||:     |    :|  :: : | | |    |:||: :|| |
Db        385 PKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVG 444

Qy        414 HEALHNHYTQKSLSLSPG 431
              ||||  ::|||::    |
Db        445 HEALPMNFTQKTIDRLSG 462


RESULT 69
Q8VEA0
ID   Q8VEA0      PRELIMINARY;      PRT;   484 AA.
AC   Q8VEA0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-VJ558 OR AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019425; AAH19425.1; -.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   484 AA;  52859 MW;  F2522DF5ED6288A6 CRC64;

  Query Match           11.0%;  Score 297.5;  DB 11;  Length 484;
  Best Local Similarity   26.1%;  Pred. No. 6.7e-16;
  Matches  111;  Conservative   56;  Mismatches  154;  Indels  105;  Gaps   21;

Qy         65 QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFG 124
              || |          | :|:  |: | |       |: ||| || |
Db         86 QGRFTI-------SRDNSQNILYLQMN------TLRAEDSATYYC--------------- 117

Qy        125 LTANSDTHLLQ-GQSLTLTLESPPGSSPSV------QCRS-------------PRG-KN 162
                 | |: :    ||  |||: | |   |::      | |                 | |  |
Db        118 ARAYSNYYFDNWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMN 177

Qy        163 I---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH--- 214
              :   : || ::       |   | :| :         :  :  | ||  |   |   |
Db        178 VTWGKSGKDITTVNFPPALASGGRYTMS-------SQLTLPAVECPEGESVKCSVQHDSN 230

Qy        215 -------TCPELLGGPSVFLFPPKPK-----------DTLMISRTPEVTCVVVDVSHED 255
                    || :   |:    || |              : |::     :|| :  :   |
Db        231 PVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RD 285

Qy        256 PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 311
              ||   | |      |    |  :::   ::   | | |||    : | :|  :|| |::
Db        286 PEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP 340

Qy        312 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG 370
                    :  ||:|       |||: |||  :||  |: |||||||: | | :: | |
Db        341 ESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN 399
```

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Qy        371 Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 425
              :   ||:     |     :|  :: : | | |    |:||: :|| | |||| ::|||:
Db        400 EELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKT 459

Qy        426 LSLSPG 431
              :    |
Db        460 IDRLSG 465


RESULT 70
Q80ZI7
ID   Q80ZI7      PRELIMINARY;      PRT;   487 AA.
AC   Q80ZI7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC049143; AAH49143.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   487 AA;  53019 MW;  31F2C893900A4D80 CRC64;

  Query Match           11.0%;  Score 297.5;  DB 11;  Length 487;
  Best Local Similarity   24.7%;  Pred. No. 6.7e-16;
  Matches  118;  Conservative   72;  Mismatches  173;  Indels  115;  Gaps   24;

Qy         30 LGKKGDTVELTCTASQKKSIQFHWKN----------SNQIKILGNQGSFLT------K 71
              | : | :::|:| ||    :   :| |              :|::  |  :: |      |
Db         30 LVQPGGSMKLSCAAS-GFTFSNYWMNWVRQSPEKGLEWVAEIRLRSN--NYATHYAESVK 86

Qy         72 GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
              |   :: | ||: |:: | |      ||: ||:  | |                |   :
Db         87 GRFTIS-RDDSKSSVYLQMN------NLRAEDTGIYYCTRR----------GYGDPNWY 128

Qy        132 HLLQGQSLTLTLESPPGSSPSV------QCRS-------------PRG-KNI---QGGK 167
                : |   |:|: | |    |::      | |               | |  |:   : ||
Db        129 FDVWGAGTTVTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGK 188

Qy        168 TLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH----------T 215
               ::       |   | :| :         :  :  | ||  |    |  |          |
Db        189 DITTVNFPPALASGGRYTMS-------SQLTLPAVECPEGESVKCSVQHDSNPVQELNVN 241

Qy        216 CPELLGGPSVFLFPPKPK-----------DTLMISRTPEVTCVVVDVSHEDPE-VKFNW 262
              || :   |:    || |             : |::     :|| :  :   |||   | |
Db        242 CPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW 296

Qy        263 YVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 319
                    |    |   :::   ::   | | |||    : | :|  :|| |::      :
Db        297 -----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTG 350

Qy        320 TISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENN 375
              ||:|       |||: |||  :||  |: |||||||: | | :: | |    :   ||:
Db        351 TIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESY 410

Qy        376 YKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                    |     :|  :: : | | |    |:||: :|| | |||| ::|||::    |
Db        411 LVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 468


RESULT 71
Q96KX8
ID   Q96KX8      PRELIMINARY;      PRT;   496 AA.
AC   Q96KX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016369; AAH16369.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53391 MW;  D346929849040D69 CRC64;

  Query Match           11.0%;  Score 297.5;  DB 4;  Length 496;
  Best Local Similarity   25.8%;  Pred. No. 6.9e-16;
  Matches  131;  Conservative   60;  Mismatches  226;  Indels   91;  Gaps   22;

Qy          8 RHLLLVLQLALLP------AATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSN 57
              :||   | |   |          | :   | |  :|: |||| |       |  : |
Db          2 KHLWFFLLLVAAPRWVLSQLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQP 61

Qy         58 QIKILGNQGSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQ 114
                | |    :    | :  |    || ::     :    | ::::   |:  | |
Db         62 PGKGLEWIANTYYSGITYYNPSLKSRVTISVDTSKNQLSLKVRSVTAADTAVYFCARHGY 121

Qy        115 KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV----QCRSPRGKN------IQ 164
                  | |    |     ||   :|: |   :|| |     | :    |       :|
Db        122 SRS------GRTGAID---YWGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQ 172

Qy        165 G---GKTLSVSQLE------------LQDSG----------TWTCTVLQNQKKVEFKI-- 197
              |    : |||:  |            ||:           |   |     | |   :
Db        173 GFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKH 232

Qy        198 ------DI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCV 247
                   |: |||| |          | |        | : |   |  :| |::     :||
Db        233 YTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCT 291

Qy        248 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              :  :  :   | | |      :  :|   | |       | | |||    : | :|| : |
Db        292 LTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCT 348

Qy        308 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEW 366
               :      |:  |:||: |    |:|: |||  :||  |: |:|||| :|| | |: | |
Db        349 AAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRW 407

Qy        367 ESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY 421
                | |   | |     : | |  :| : | | |    |::|: ||| | ||||   :
Db        408 LQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAF 467

Qy        422 TQKSLSLSPG----------LQLDETC 438
              |||::    |          ::| ||
Db        468 TQKTIDRLAGKPTHVNVSVVMAEVDGTC 495
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RESULT 72
Q8NCL6
ID   Q8NCL6       PRELIMINARY;      PRT;   493 AA.
AC   Q8NCL6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ90170.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mammary gland;
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK074651; BAC11114.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   493 AA;  53224 MW;  12ECD7E094777101 CRC64;

  Query Match             10.9%;  Score 295;  DB 4;  Length 493;
  Best Local Similarity   25.4%;  Pred. No. 1.1e-15;
  Matches  125;  Conservative   67;  Mismatches  196;  Indels  104;  Gaps   24;

Qy         25 GNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQ------IKILGNQG-----SFLTK 71
Db         27 GGGVVL--PGGSLRLSCAASGFRFRDYDMHWVRQSPGEGLEWVALIWYDGTKTYYSDSVK 84

Qy         72 GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
Db         85 GRLTVS-RDNYKNTLY------LEMKSLGAEDTAVYYC-ARDQ----GYAGYGVF----D 128

Qy        132 HLLQGQSLTLTLESP--------------PGSSPSVQC---------------------- 155
Db        129 HWGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGV 188

Qy        156 ---RSPRGKNIQGGKTLSVSQLELQDS-----GTWTCTVLQNQKKVEFKIDI-VPCPAPE 206
Db        189 TARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQ---DVTVPCPVPS 245

Qy        207 PKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 263
Db        246 TPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWT 303

Qy        264 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
Db        304 PSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 361

Qy        324 AKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTP 380
Db        362 S-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWA 420

Qy        381 PVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------ 431
Db        421 SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVN 480

Qy        432 -----LQLDETC 438
Db        481 VSVVMAEVDGTC 492


RESULT 73
Q91WR1
ID   Q91WR1       PRELIMINARY;      PRT;   488 AA.
AC   Q91WR1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-VJ558 OR AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013539; AAH13539.1; -.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   488 AA;  52964 MW;  F12068460B400B9D CRC64;

  Query Match             10.8%;  Score 293;  DB 11;  Length 488;
  Best Local Similarity   24.1%;  Pred. No. 1.6e-15;
  Matches  113;  Conservative   73;  Mismatches  188;  Indels   94;  Gaps   23;

Qy         30 LGKKGDTVELTCTASQKKSIQFH--W---KNSNQIKILGNQGSFLTKGPSKLNDRADSRR 84
Db         30 LVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEWIGDINPY--NGGTSYNQKFKGKA 87

Qy         85 SLWDQGNFPLI---IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL 141
Db         88 TLTVDKSSSIAYMQLNNLTSDDSAVYYC----ARGPVYYSYF----SYDRGDYWGQGTLV 139

Qy        142 TLESPPGSSPSV------QCRS-------------PRG-KNI---QGGKTLSVSQL--E 175
Db        140 TVSAEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPA 199

Qy        176 LQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH----------TCPELLGGPSV 225
Db        200 LASGGRYTMS-------SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGICSPPTT 252

Qy        226 FLFPPKPK------------DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNA 272
Db        253 ---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTG 302

Qy        273 KTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329
Db        303 KDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTF 361

Qy        330 EPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDS 385
Db        362 PPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPG 421

Qy        386 DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        422 EGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 469
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RESULT 74
Q8N5K4
ID   Q8N5K4      PRELIMINARY;      PRT;   499 AA.
AC   Q8N5K4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032249; AAH32249.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   499 AA;  53376 MW;  93A5C89582054F32 CRC64;

  Query Match             10.7%;  Score 290;  DB 4;  Length 499;
  Best Local Similarity   26.1%;  Pred. No. 2.9e-15;
  Matches  129;  Conservative   65;  Mismatches  197;  Indels  104;  Gaps   24;

Qy         25 GNKVVLGKKGDTVELTCTAS-------------QKKSIQFHWKNSNQIKILGNQGSF--- 68
              |  ||  : | :: |:|  |               |      | :|    |  | ||
Db         27 GGGVV--RPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSS----INWNGGSTNYA 80

Qy         69 -LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA 127
               ||   :: | ::: ||: | |      :|::||:  | |  :  |       |
Db         81 DSVKGRFTIS-RDNAKNSLYLQMN------SLRVEDTALYYCARDPTKYCSGGSCLGYYM 133

Qy        128 NSDTHLLQGQSLTLTLESPPGSSPSV----QCRSPRGKN------IQG---GKTLSVSQL 174
              :     : |:  |:|: |   :|| |     | :    |      :||    : |||:
Db        134 D-----VWGKGTTVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWS 188

Qy        175 E------------LQDSG----------TWTCTVLQNQKKVEFKI--------DI-VPCP 203
              |            ||:          |   |     | |   :         |: ||||
Db        189 ESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCP 248

Qy        204 APEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
              |       | |       | : |  |  :| |::     :|| :  :  :   | |
Db        249 VPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTF 306

Qy        261 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 320
              |     :  :|   | :      | | |||    : | :|| : |  :      |:  |
Db        307 TWTPSSGK--SAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTAT 364

Qy        321 ISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYK 377
              :||: |    |:|: |||  :||  |: |:|||| :|| | |: | |     |  |   |
Db        365 LSKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYL 423

Qy        378 TTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG--- 431
              |     : | |  :| : | | |    |::|: ||| | ||||   :|||::   |
Db        424 TWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPT 483

Qy        432 --------LQLDETC 438
                      ::| ||
Db        484 HVNVSVVMAEVDGTC 498
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RESULT 75
Q96DK0
ID   Q96DK0      PRELIMINARY;      PRT;   496 AA.
AC   Q96DK0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ25298.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gastric mucosa;
RA   Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA   Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA   Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA   Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK058027; BAB71633.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   496 AA;  53532 MW;  C72EE1E247C86FED CRC64;

  Query Match             10.6%;  Score 287.5;  DB 4;  Length 496;
  Best Local Similarity   26.0%;  Pred. No. 4.6e-15;
  Matches  126;  Conservative   63;  Mismatches  193;  Indels  103;  Gaps   25;

Qy         34 GDTVELTCTASQK--KSIQFHWKNSNQIKILGNQGSFLTK--GPS---KLNDRA-----D 81
              | :|:::| ||    :|  | |       : |   |  :      |:      ||     |
Db         34 GSSVKVSCKASANMFRSYAFTWVRQAPGQGLQWMGGIIPNFGAPNYAQNFQDRVTISADD 93

Qy         82 SRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLT--ANSDTHLLQ--GQ 137
              |  :::       : : :|  ||:  | |                |||   :  : ||  ||
Db         94 STTTVY------MELTSLTFEDTAFYYCG------------RGLTYYGSGSYYYLQHWGQ 135

Qy        138 SLTLTLESPPGSSPSV----QCRSPRGKN------IQG---GKTLSVSQLE--------- 175
                :|: |   :|| |     | :    |      :||    : |||: |
Db        136 GTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARN 195

Qy        176 ---LQDSG----------TWTCTVLQNQKKVEFKI--------DI-VPCPAPEPKSCDKT 213
                 ||:          |   |     | |   :         |: |||| |
Db        196 FPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSP 255

Qy        214 HTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 270
              | |       | :  |  :| |::     :|| :  :  :   | | |     :
Db        256 STPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK-- 311

Qy        271 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 330
              :|   | :      | | |||    : | :|| : |  :      |:  |:||: |
Db        312 SAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFR 370

Qy        331 PQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SD 386
              |:|: |||  :||  |: |:|||| :|| | |: | |     |  |   | |     : |
Db        371 PEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQ 430

Qy        387 G--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----------LQ 433
              |  :| : | | |     |::|: ||| | ||||   :|||::    |           :
Db        431 GTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAE 490

Qy        434 LDETC 438
              :| ||
Db        491 VDGTC 495
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RESULT 76
Q9DCD9
ID   Q9DCD9      PRELIMINARY;      PRT;   426 AA.
AC   Q9DCD9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Adult male kidney cDNA, RIKEN full-length enriched library,
DE   clone:0610041A01, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK002875; BAB22422.1; -.
DR   PIR; F33932; F33932.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
SQ   SEQUENCE   426 AA;  45819 MW;  56E1275BA48F6FB1 CRC64;

  Query Match             10.6%;  Score 286.5;  DB 11;  Length 426;
  Best Local Similarity   26.8%;  Pred. No. 4.5e-15;
  Matches  106;  Conservative   58;  Mismatches  140;  Indels   91;  Gaps   18;

Qy         96 IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP------PGS 149
              : :|  |||  | |   |        :   :|          || |:|:: ||        | :
Db         45 LSSLTSEDSAVYFCARSDYYGPYAMDYWG----------QGTSVTVSSESARNPTIYPLT 94

Qy        150 SPSVQCRSP---------------------RGKNIQ-----------GGKTLSVSQL-- 174
               |        |                      ||:|             || |:| |||
Db         95 LPRALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTL 153

Qy        175 ---ELQDSGTWTCTVLQNQKKVEFKIDI------VPCPAPEPKSCDKTHTCPELLGGPSV 225
                 |  :  :  |:|  :   |: ::|:       ||| | | ||            ||:
Db        154 PAVECPEGESVKCSVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH-----------PSL 200

Qy        226 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST- 284
               |  |  :| |::      :|| :  : : :  | | |     |     |    :::    ::
Db        201 SLQRPALED-LLLGSDASLTCTLNGLRNPEGAV-FTW-----EPSTGKDAVQKKAVQNSC 253

Qy        285 --YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 342
                | | |||     :  | :|   :|| |::       :   ||:|        |||: ||| :|
Db        254 GCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKITVNTFPPQVHLLPPPSEE 312

Qy        343 LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLT 396
              |  |: ||||||: | | :: | |     :    ||:      |        :|  :: : | |
Db        313 LALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLR 372

Qy        397 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              |      |:||: :|| | ||||   ::|||::     |
Db        373 VSAELWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 407

RESULT 77
Q91WP5
ID   Q91WP5      PRELIMINARY;      PRT;   479 AA.
AC   Q91WP5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013656; AAH13656.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51603 MW;  ECB2D0877748584F CRC64;

  Query Match             10.6%;  Score 286.5;  DB 11;  Length 479;
  Best Local Similarity   24.0%;  Pred. No. 5.3e-15;
  Matches  126;  Conservative   80;  Mismatches  160;  Indels  159;  Gaps   29;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQ----GNKVVLGKKGDTVELTCTAS------------ 44
              || |:      : |||  |   :       |     |  :|   | | :::::| ||
Db          1 MNFGLTL--IFLVLTLKGVQCEVQLVESGGGLV--KPGGSLKVSCAASGLTFSNYAMSWV 56

Qy         45 -QKKSIQFHWK---NSNQIKILGN-------QGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
               |     :   |        |||     ||           :| |             | ::: :|:
Db         57 RQSPEKRLEWVAAINSNG----GNTYYSDTMKGRFTI-------SRDNAKSTLY------ 99

Qy         94 LIIKNLKIEDSDTYIC-----------------EVEDQKE-EVQLLVFGLTANSDTHLL- 134
              | : :|: ||:  | |                    | :|   :   |  |      :||  ::
Db        100 LQMSSLRSEDTAFYYCVRGGYFDVWGAGTAVTVSSEPAREPTIYPLTFPQALSSDPVIIG 159

Qy        135 ------------------QGQSLTLTLESPPG-------------SSPSVQCRSPRGKNI 163
                                |: :| |:  ||                  : |:|:|  | |:::
Db        160 CLIHDYFPSGTMNVTWGKSGKDIT-TVNFPPALASGGRYTMSSQLTLPAVEC--PEGESV 216

Qy        164 QGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCP-------APEPKSCDKTHTC 216
              :                   |:|     |: :::  | ||                | | ||
Db        217 K------------------CSVQHDSNPVQ-ELN-VNCPGICSPPTTPPPSCQ----- 250

Qy        217 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTK 275
                    ||:  | |    :| |:     :|| :  |   |||   | ||          |       |
Db        251 ------PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTGKDA 296

Qy        276 PREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
              :::    ::    |  | |||    :  | :|   :|| |::        :    ||:|         ||
Db        297 VQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQ 355

Qy        333 VYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG- 387
              |: :||  :||  |: ||||||: | | :: | |      :    ||:       |        :|
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Db        356 VHLIPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGA 415

Qy        388 -SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        416 TTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 460


RESULT 78
Q7TMK4
ID   Q7TMK4      PRELIMINARY;      PRT;   479 AA.
AC   Q7TMK4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055905; AAH55905.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  52209 MW;  532DED9D46D0AEED CRC64;

  Query Match             10.5%;  Score 284.5;  DB 11;  Length 479;
  Best Local Similarity   24.4%;  Pred. No. 7.7e-15;
  Matches  117;  Conservative   68;  Mismatches  168;  Indels  127;  Gaps   20;

Qy         30 LGKKGDTVELTCTAS-------------------------QKKSIQFHWKNSNQIKILG 63
Db         30 LVQPGRPMKLSCVASGFTFGDYWMNWVRQSPEKGLEWVSQIRNKPYNYETYYSDSVK--- 86

Qy         64 NQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF 123
Db         87 --GRFTI-------SRDDSKSGVYLQMN------NLRPEDMGIYYCTVEGM--------- 122

Qy        124 GLTANSDTHLLQGQSLTLTLES-----------PPGSS--------------PSVQCRSP 158
Db        123 -------DYWGRGISVTVSSESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVT 175

Qy        159 RGKN-------------IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVEFKIDIV 200
Db        176 WGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-V 233

Qy        201 PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
Db        234 NCSGPTPPPPITIPSCQ-----PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-F 286

Qy        261 NWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 317
Db        287 TW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTL 340

Qy        318 EKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PE 373
Db        341 TGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGNEELSPE 400

Qy        374 NNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        401 SYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 460


RESULT 79
Q8VCV5
ID   Q8VCV5      PRELIMINARY;      PRT;   481 AA.
AC   Q8VCV5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018455; AAH18455.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   481 AA;  52326 MW;  52B44C5826807143 CRC64;

  Query Match             10.5%;  Score 284.5;  DB 11;  Length 481;
  Best Local Similarity   25.5%;  Pred. No. 7.8e-15;
  Matches  119;  Conservative   67;  Mismatches  182;  Indels   99;  Gaps   21;

Qy         30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILG--------NQGSFLT---KGPSKL 76
Db         30 LVRPGTSVKVSCKASGYSFIDYNIYWVKQSHGKSLEWIGYIDPYNGGSSYNQKFKGKATL 89

Qy         77 NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
Db         90 TVDKSSNTAF-------MYLNNLTSEDSAFYYCARE--WYGAWFAFWG----------QG 130

Qy        137 QSLTLTLES-----------PPGSS--------------PSVQCRSPRGKN--------- 162
Db        131 TLVTVSAESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNF 190

Qy        163 ----IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT 213
Db        191 PPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-VNCSGPTPPPPITI 248

Qy        214 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
Db        249 PSCQ-----PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-FTW-----EPSTGK 296

Qy        274 TKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 330
Db        297 DAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIAKVTVNTFP 355

Qy        331 PQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSD 386
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Db        356 PQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGE 415

Qy        387 G--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
Db        416 GATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 462


RESULT 80
Q8WY24
ID   Q8WY24      PRELIMINARY;      PRT;   497 AA.
AC   Q8WY24;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   SNC66 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT   "Identification and characterization of SNC66, a Ig-like gene which is
RT   down-regulated in colorectal cancer.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF283666; AAL36987.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   497 AA;  53665 MW;  F24D08DFA5A663E5 CRC64;

  Query Match             10.5%;  Score 284;  DB 4;  Length 497;
  Best Local Similarity   25.2%;  Pred. No. 8.9e-15;
  Matches  129;  Conservative   65;  Mismatches  213;  Indels  104;  Gaps   23;

Qy         11 LLVLQLALLPAATQ------GNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGN 64
Db          7 LLFLVAAVTSAHSQEQLEQSGAEVT--KPGASVKVSCKASGYTFIAY---DINWVRQAPG 61

Qy         65 QG--------------SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICE 110
Db         62 QGLEWMGWMNPQTGNTEFAQKFQGRLTFSRDT-----SINTAYMVLSSLSTEDSAIYFCA 116

Qy        111 ------------------------VEDQKEEVQLLVFGLTANSD--------THLLQG-- 136
Db        117 RGNLRGGRGFGYNWFDPWGHGTLVTVSSASPTNPKVFPLSLCSTQPDGNVVIACLVQGFF 176

Qy        137 --QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLELQDS-----GTWTCTVLQ 188
Db        177 PQEPLSVTWSE---SGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKH 233

Qy        189 NQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEV 244
Db        234 YTNPSQ---DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANL 289

Qy        245 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 304
Db        290 TCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTF 346

Qy        305 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIA 363
Db        347 TCTAAYPESKTPLTATLPKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVL 405

Qy        364 VEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 418
Db        406 VRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALP 465

Qy        419 NHYTQKSLSLSPG-----------LQLDETC 438
Db        466 LAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC 496


RESULT 81
Q9UP60
ID   Q9UP60      PRELIMINARY;      PRT;   384 AA.
AC   Q9UP60;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   SNC73 protein.
GN   SNC73.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng S., Cao J., Cao W., Cai X., Geng L.;
RT   "Identification and characterization of SNC73, a gene which is down-
RT   regulated in colorectal cancer.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF067420; AAC19365.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   384 AA;  40947 MW;  BA7ADC3CA5A9DD48 CRC64;

  Query Match             10.4%;  Score 281.5;  DB 4;  Length 384;
  Best Local Similarity   26.6%;  Pred. No. 1e-14;
  Matches  107;  Conservative   51;  Mismatches  155;  Indels   89;  Gaps   19;

Qy         87 WDQGN--------------FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF------GLT 126
Db         21 WGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVT 80

Qy        127 ---------ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ 177
Db         81 ARNFPPSQDASGDLYTTSSQ---LTL-------PATQCLA--GKSV-------------- 114

Qy        178 DSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKPK 233
Db        115 -----TCHVKHYTNPSQ---DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALE 166

Qy        234 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 293
Db        167 D-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPG 222

Qy        294 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTC 352
Db        223 CAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTC 281

Qy        353 LVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNV 407
Db        282 LARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDT 341

Qy        408 FSCSVMHEALHNHYTQKSLSLSPG-----------LQLDETC 438
Db        342 FSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC 383


RESULT 82
Q99M22
ID   Q99M22      PRELIMINARY;      PRT;   479 AA.
AC   Q99M22;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002091; AAH02091.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  51992 MW;  768E39A138918892 CRC64;

  Query Match             10.4%;  Score 281;  DB 11;  Length 479;
  Best Local Similarity   23.2%;  Pred. No. 1.5e-14;
  Matches  115;  Conservative   82;  Mismatches  184;  Indels  114;  Gaps   23;

Qy          9 HLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS-QKKSIQFHWKNSNQIKILGNQ-- 65
              :||  :   |      | :   | |   :: |||: :    :  ::|    |    ||:
Db          8 YLLTAIPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFP--GNKLE 65

Qy         66 --GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYIC---------- 109
                |      | :  |    :| |:      :  | | : ::  ||: || |
Db         66 WMGYINYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASRGYSWFPNW 125

Qy        110 --------EVEDQKEEVQLLVFGLT----ANSDTHLL------------------QGQS 138
                      |  :      :: ||     :|| ::                      |:
Db        126 GQGTLVTVSAESARNPT---IYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKD 182

Qy        139 LTLTLESPPG-------------SSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCT 185
              :| |:  ||               : |:|:|  | |:::                    |:
Db        183 IT-TVNFPPALASGGRYTMSSQLTLPAVEC--PEGESVK------------------CS 220

Qy        186 VLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVT 245
              |  :   |: ::| | |  | |       :|      ||: |  |  :| |::     :|
Db        221 VQHDSNPVQ-ELD-VNCSGPTPPPPITIPSCQ-----PSLSLQRPALED-LLLGSDASIT 272

Qy        246 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGK 302
              | :  : : :  | | |     |   |  :::   ::   | | |||    : | :|
Db        273 CTLNGLRNPEGAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGA 326

Qy        303 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSD 361
               :|| |::      :  ||:|       |||: |||  :||  |: :||||||: | | :
Db        327 SFKCTVTHPE-SGTLTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVRAFNPKE 385

Qy        362 IAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
              : | |    :   ||:     |     :|  :: : | | |    |:||: :|| | |||
Db        386 VLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEA 445

Qy        417 LHNHYTQKSLSLSPG 431
              |  ::|||::    |
Db        446 LPMNFTQKTIDRLSG 460


RESULT 83
Q29028
ID   Q29028      PRELIMINARY;      PRT;    99 AA.
AC   Q29028;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD4, allele 2 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=#1183; TISSUE=Blood;
RX   MEDLINE=93329116; PubMed=8335933;
RA   Gustafsson K., Germana S., Sundt T.M., Sachs D.H., LeGuern C.;
RT   "Extensive allelic polymorphion in an exposed region of the
RT   miniature. . . . . .";
RL   J. Immunol. 151:1365-1370(1993).
DR   EMBL; X65630; CAA46584.1; -.
DR   PIR; I47132; S21462.
DR   HSSP; P01730; 1CDY.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  11390 MW;  C229E5BEA228318F CRC64;

  Query Match             10.4%;  Score 280.5;  DB 6;  Length 99;
  Best Local Similarity   56.1%;  Pred. No. 1.8e-15;
  Matches   55;  Conservative   19;  Mismatches   23;  Indels    1;  Gaps    1;

Qy         32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGP-SKLNDRADSRRSLWDQG 90
              | ||  || | :||||:: | ||||:|||||  :  :   |   ::|: | ||::::|| |
Db          1 KAGDLAELPCHSSQKKNLPFSWKNSDQIKILRSHRNLWHKASVTELSSRLDSKKNMWDHG 60

Qy         91 NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN 128
              :|||||||:: ||  |||||||:: |||||| |||:
Db         61 SFPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS 98


RESULT 84
Q9BRV0
ID   Q9BRV0      PRELIMINARY;      PRT;   500 AA.
AC   Q9BRV0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005951; AAH05951.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   500 AA;  54154 MW;  0A9BF43F2A3CC6D9 CRC64;

  Query Match             10.1%;  Score 273.5;  DB 4;  Length 500;
  Best Local Similarity   25.8%;  Pred. No. 6.6e-14;
  Matches  104;  Conservative   56;  Mismatches  154;  Indels   89;  Gaps   19;

Qy         86 LWDQGN--------------FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF------GL 125
              :| :|                |||  : : : : :    | |:    :  | |       |:
Db        136 VWGKGTTVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGV 195

Qy        126 T---------ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
```

```
Db        196 TARNFPPSQDASGDLYTTSSQ---LTL-------PATQCLA--GKSV------------ 230

Qy        177 QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKP 232

Db        231 ------TCHVKHYTNPSQ---DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPAL 281

Qy        233 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292

Db        282 ED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLS 337

Qy        293 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLT 351

Db        338 GCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLT 396

Qy        352 CLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGN 406

Db        397 CLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGD 456

Qy        407 VFSCSVMHEALHNHYTQKSLSLSPG-----------LQLDETC 438

Db        457 TFSCMVGHEALPLAFTQETIDRLAGKPTHVNVSVVMAEVDGTC 499


RESULT 85
Q8K0Z4
ID   Q8K0Z4      PRELIMINARY;      PRT;   480 AA.
AC   Q8K0Z4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to expressed sequence AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029188; AAH29188.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
SQ   SEQUENCE   480 AA;  51645 MW;  8690A63C669CDBED CRC64;

  Query Match             10.0%;  Score 270;  DB 11;  Length 480;
  Best Local Similarity   24.7%;  Pred. No. 1.2e-13;
  Matches  116;  Conservative   71;  Mismatches  178;  Indels  104;  Gaps   22;

Qy         30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG----SFLT--KGPSKLNDRAD 81

Db         30 LVKPGALVKISCKASGYTFTSFDISW-----MKQRPGQGPEWIGWISPGDGSSEYNEKFK 84

Qy         82 SRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSD----THLL 134

Db         85 GKATLTADKSSNTAYMHLSSLTSENSAVYFC----------------ARSKLGGFAYWG 127

Qy        135 QGQSLTLTLES-----------PPGSS--------------PSVQCRSPRGKN------- 162

Db        128 QGTLVTVSAESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTV 187

Qy        163 ------IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211

Db        188 NFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-VNCSGPTPPPPI 245

Qy        212 KTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 271

Db        246 TIPSCQ-----PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-FTW-----EPST 293

Qy        272 AKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 328

Db        294 GKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIAKVTVNT 352

Qy        329 REPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLD 384

Db        353 FPPQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEP 412

Qy        385 SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431

Db        413 GEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG 461


RESULT 86
Q8WU38
ID   Q8WU38      PRELIMINARY;      PRT;   573 AA.
AC   Q8WU38;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC021276; AAH21276.1; -.
DR   PIR; S21205; S21205.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   573 AA;  62967 MW;  FD072344033AC530 CRC64;

  Query Match             7.2%;  Score 193.5;  DB 4;  Length 573;
  Best Local Similarity   21.3%;  Pred. No. 3.1e-07;
  Matches  129;  Conservative   65;  Mismatches  192;  Indels  221;  Gaps   28;

Qy          1 MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKN 55

Db          1 MELGLSWIFLLAILKGVQCEVQLVESGGGLV---QPGRSLRLSCAASGFTFDDYAMHWVR 57

Qy         56 SNQIK-------ILGNQGSF----LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDS 104

Db         58 QAPGKGLEWVSGISWNSGSIGYADSVKGRFTIS-RDNAKNSLYLQMN------SLRAEDT 110

Qy        105 DTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQ 164

Db        111 ALYYCAKHGSGSYI-----GYYYGMD---VWGQGTTVTVSSAPTKAPDV----------- 151

Qy        165 GGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS 224

Db        152 ------------------------------FPI-ISGCRHPKDNS------------PV 167

Qy        225 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 284

Db        168 V------------------LACLI--TGYHPTSVTVTWYM-GTQSQPQRTFPEIQRRDSY 206

Qy        285 YRVVSVLTVLHQDWLNGKEYKCKVSN-------------------------------- 310
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                |   | |:   | |  | |||| | :
Db        207 YMTSSQLSTPLQQWRQG-EYKCVVQHTASKSKKEIFRWPESPKAQASSVPTAQPQAEGSL 265

Qy        311 -KALPAPI----------EKTISKAKGQPREPQ--------------VYTLPPSRDEL-T 344
               ||  ||            ||   | | :  | :             || | |:  :|
Db        266 AKATTAPATTRNTGRGGEEKKKEKEKEEQEERETKTPECPSHTQPLGVYLLTPAVQDLWL 325

Qy        345 KNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 403
               ::: : || | |    |  : ||  |: |    :          |:||   :|:||: :| |
Db        326 RDKATFTCFVVGSDLKDAHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWN 385

Qy        404 QGNVFSCSVMHEALHNHYTQKSLSLSPG--LQLDETCAEAQ-DGELDGLWTTDPPRASAL 460
               |   :|:: |             || |   : | |  |:|     |: | ::||| |::
Db        386 AGTSVTCTLNHP-----------SLPPQRLMALREPAAQAPVKLSLNLLASSDPPEAASW 434

Qy        461 P-------APPT----------------GSALPDPQTASA---------LPDPPAASAL 487
                      :||                | | ||  |           :| ||  |
Db        435 LLCEVSGFSPPNILLMWLEDQREVNTSGFAPARPPPQPGSTTFWAWSVLRVPAPP--SPQ 492

Qy        488 PAALAVI 494
               ||   :
Db        493 PATYTCV 499


RESULT 87
Q90WB5
ID   Q90WB5      PRELIMINARY;      PRT;   482 AA.
AC   Q90WB5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor.
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Chan S.W.S., Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF378701; AAK59279.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL       1     29       POTENTIAL.
SQ   SEQUENCE   482 AA;  54624 MW;  BDA0E8EC6172AD0B CRC64;

  Query Match             7.0%;  Score 189;  DB 13;  Length 482;
  Best Local Similarity   22.2%;  Pred. No. 5.7e-07;
  Matches   95;  Conservative   70;  Mismatches  148;  Indels  114;  Gaps   22;

Qy          8 RHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWK-------NSNQIK 60
              | : ::||| |       ::  :| :|  | | |   :|      ||       ::  |:
Db         12 RAVFVLLQLGL--THIMAHQQQIGVEGKEVILNC---KKHDKDVTWKYEYDAGSSAIIIQ 66

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||  :   : || : ::||:::     :| :  | : ||:| |: ||||    :  : |
Db         67 ILAGK---IFKGRAPMSDRSET-----NQNSKHLKVSNLRISDAGTYICECGSDRNSISL 118

Qy        121 LVFGLTANSDTHLLQGQSLTLT-LESPPGSSPS----------------VQCRSPRGKN 162
               |  || :|: : | |  | || :   | | |                 :|  :|:
Db        119 HVVKLTISSNGYFLPGDDLELTVMHKSPKSQPRFSITLFNSHNSRVTPEVLQNETPQ--- 175

Qy        163 IQGGKTLSVSQLELQDSGTWTCTVLQN----QKKVEFKIDIVPCPAPEPKSCDKTH---- 214
                | | ||:  ||||| | :  :     : : | : ::          :|||
Db        176 ---KYALKVKQLQPTDSGTWICNMHSDSPSINENISFNVKVL--------GFEKTHLERM 224

Qy        215 --------TCP-----ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 261
                       |         :|    |         |       :|  ::|          ||
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Db        225 YAAVDSTVTLSWHLNFRKIGWKEFF------TGQLNWQEGNAITYELLD---------FN 269

Qy        262 WYVDGVEVHNAKTKPR------EEQYNSTYRVVSVLTVLHQDWL-NGKEYKCKV--SNKA 312
                 || |:   | : :      | : :||  |      :|:  | :  || |::  : :
Db        270 ATADG-ELRETKKRSQALLEIPEMKRDSTVEV-----KIHKIQLKHSGEYTCQLLYNRRY 323

Qy        313 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES-NGQ 371
               : :  |  : :     |  |    ||         :::| | |    | :: : ||  ||
Db        324 IQSKTELVVMQVSANPPGP----LPKGA------EMTLLCQVSSPIPPNVHLLWERVNGT 373

Qy        372 PENNYKT 378
               :  |:
Db        374 KMDGKKS 380


RESULT 88
Q90524
ID   Q90524      PRELIMINARY;      PRT;   268 AA.
AC   Q90524;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Novel antigen receptor (Fragment).
OS   Ginglymostoma cirratum (Nurse shark).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC   Ginglymostomatidae; Ginglymostoma.
OX   NCBI_TaxID=7801;
RN   [1]
RP   SEQUENCE OF 1-240 FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=95183140; PubMed=7877689;
RA   Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA   Flajnik M.F.;
RT   "A new antigen receptor gene family that undergoes rearrangement and
RT   extensive somatic diversification in sharks.";
RL   Nature 374:168-173(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Greenberg A.S.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U18680; AAB48352.1; -.
DR   HSSP; P01842; 7FAB.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Receptor.
FT   NON_TER     268    268
SQ   SEQUENCE   268 AA;  29579 MW;  0CDE524DD6E9FDC4 CRC64;

  Query Match             6.9%;  Score 186;  DB 13;  Length 268;
  Best Local Similarity   24.3%;  Pred. No. 4.4e-07;
  Matches   65;  Conservative   39;  Mismatches   98;  Indels   66;  Gaps   10;

Qy        223 PSVFLFPPKPKDTLMISRTPE-----------VTCVVVDVSHEDPEVKFNWYVDG----- 266
              | ||         |  : :||:           : ||: | :   |   :|    |
Db         14 PYVF--------TARVDQTPQEITKETGESLSINCVLRDSNCALPSTYWNRKKSGSTNEE 65

Qy        267 --------VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV--SNKALPAP 316
                     ||  |: :|   : |       |||      :   |:|||   | |
Db         66 TISKGGRYVETVNSGSKSFSLRIND-------LTV-----EDSGTYRCKVYRKNWAYDCG 113

Qy        317 IEKT-----------ISKAKGQPREPQVYTL--PPSRDELTKNQVSLTCLVKGFYPSDIA 363
              :|:            ::   | |  | : :|    : ::     | | ||: |:|| :||
Db        114 LEELDWIYVYGGGTGVTVNPGIPLSPPIVSLLHSATEEQRANGFVQLVCLISGYYPENIA 173

Qy        364 VEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT 422
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                 | |: | :   : : || ||  |   |   | | |    | :|:|:|| | | |  ::
Db        174 VSWQKNTKTITSGFATTSPVKTSSNDFSCASLLKVPLQEWSRGSVYSCQVSHSATSSNQR 233

Qy        423 QKSLSLSPGLQLDETCAEAQDGELDGLW 450
              ::  | |      |     :|  :: :|
Db        234 KEIRSTS------EIAVLLRDPTVEEIW 255


RESULT 89
Q9D8W4
ID   Q9D8W4      PRELIMINARY;      PRT;   130 AA.
AC   Q9D8W4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1810027O01Rik protein.
GN   1810027O01RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007622; BAB25142.1; -.
DR   PIR; S22760; S22760.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:1916426; 1810027O01Rik.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   130 AA;  14253 MW;  438197975E766E54 CRC64;

  Query Match             6.8%;  Score 183.5;  DB 11;  Length 130;
  Best Local Similarity   36.5%;  Pred. No. 2.5e-07;
  Matches   38;  Conservative   18;  Mismatches   43;  Indels    5;  Gaps    3;

Qy        326 GQPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVL 383
              |||:  | |   ||| :||  |: :| | :  |||  : |:|: :| |     :|| |
Db         25 GQPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSK 84

Qy        384 DSDGSPFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
               |:  :   | ||:    |:: : :|| | ||    |  :||||
Db         85 QSNNKYMASSYLTLTARAWERHSSYSCQVTHE---GHTVEKSLS 125


RESULT 90
Q8N355
ID   Q8N355      PRELIMINARY;      PRT;   234 AA.
AC   Q8N355;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028090; AAH28090.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  24792 MW;  CC848CAEBA4A9D63 CRC64;

  Query Match             6.8%;  Score 183.5;  DB 4;  Length 234;
  Best Local Similarity   25.0%;  Pred. No. 5.8e-07;
  Matches   55;  Conservative   39;  Mismatches   99;  Indels   27;  Gaps    7;

Qy        210 CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY------ 263
              |  : |   |  |||  : |          :|  :||   ::  :      :||
Db         14 CTGSVTSYVLTQPPSVSVAP---------GQTARITCGGNNIGSK----SVHWYQQKPGQ 60

Qy        264 VDGVEVHNAKTKPR---EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI--- 317
               : |::  :|   |   |     : ||:   |  :  :| |:: : :   |:
Db         61 APVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVDAGDEADYYCQLWDSSSDHPVVFG 120

Qy        318 EKTISKAKGQPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENN 375
              |    |||:  | |   ||| :||  |: :| ||:  |||  : | |:::  | :
Db        121 GGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

Qy        376 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
               :|| |   |:  :   | |::   :|:    :|| | ||
Db        181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE 220


RESULT 91
Q99M11
ID   Q99M11      PRELIMINARY;      PRT;   235 AA.
AC   Q99M11;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002129; AAH02129.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
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DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25403 MW;  39807BFE6782A3FB CRC64;

  Query Match             6.8%;  Score 183.5;  DB 11;  Length 235;
  Best Local Similarity   24.9%;  Pred. No. 5.9e-07;
  Matches   58;  Conservative   39;  Mismatches  101;  Indels   35;  Gaps    9;

Qy        213 THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY--------- 263
              | :| :|:      |  |    |  :  | :: |     :  |  |  |||
Db         15 TGSCAQLV------LTQPSSVST-SLGSTAKLPCKASTGNIGDSYV--NWYQQYMGRSPT 65

Qy        264 --VDGVEVHNAKTKPR-----EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 316
                : | ::  :    |     :   || :    ||: :    :  :| |:  :  :
Db         66 NMIYGDDLRPSGVSDRFSGSIDSSSNSAF-----LTIQNVQADDEADYYCQSYSSGIRVF 120

Qy        317 IEKTISKAKGQPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-EN 374
              |     ||:  | |   ||| :||  |: :| | :  |||  : |:|:::| |
Db        121 GGGTKLTVLSQPKTSPSVTLFPPSSEELETNKATLVCTISDFYPGVVTVDWKADGTPVTQ 180

Qy        375 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
               :|| |   ::  :  | ||:    |:  : :|| | ||    |  :||||
Db        181 GVETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHE---GHTVEKSLS 230


RESULT 92
Q7Z3Y4
ID   Q7Z3Y4      PRELIMINARY;      PRT;   236 AA.
AC   Q7Z3Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25702 MW;  7FBFE4ED23084BC6 CRC64;

  Query Match             6.7%;  Score 182;  DB 4;  Length 236;
  Best Local Similarity   23.1%;  Pred. No. 7.8e-07;
  Matches   75;  Conservative   36;  Mismatches  107;  Indels  106;  Gaps   10;

Qy         11 LLVLQLALLPAA------TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGN 64
              || | |   | |      ||     :    |||| :|| |||  |    |         |
Db          9 LLGLLLLCFPGARCDIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKP----GK 64

Qy         65 QGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF 123
                  | | | |      |: |    | :| | | :|: ||  || |:
Db         65 APKSLIYGASSLQSGVQSKFSGSGSGTDFTLTISSLQPEDFATYYCQ------------- 111

Qy        124 GLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT 183
                        | :|  :|                                      ||
Db        112 -----------QYKSYPVTF---------------------------------GQGT-- 124

Qy        184 CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPE 243
                    |:| |                      :  ||||:||  | |  : | |
Db        125 --------KLEIK--------------------RTVAAPSVFIFP--PSDEQLKSGTAS 153

Qy        244 VTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 301
              | |:: :      | |  | ||      :: ::   ::  :||| : | ||:   |:
Db        154 VVCLLNNFYPR--EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH 211

Qy        302 KEYKCKVSNKALPAPIEKTISKAK 325
              | | |:|::: | :|: |: :: :
Db        212 KVYACEVTHQGLSSPVTKSFNRGE 235


RESULT 93
Q7Z3B9
ID   Q7Z3B9      PRELIMINARY;      PRT;   398 AA.
AC   Q7Z3B9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein DKFZp686A05192.
GN   DKFZP686A05192.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RA   Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX537992; CAD97951.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   398 AA;  43260 MW;  DF82E30734B1246F CRC64;

  Query Match             6.7%;  Score 181.5;  DB 4;  Length 398;
  Best Local Similarity   23.8%;  Pred. No. 1.8e-06;
  Matches   92;  Conservative   54;  Mismatches  158;  Indels   83;  Gaps   16;

Qy        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKV 193
              |    |       |  | |   |   |      :: :| :   |:||: |   :  :   |
Db         72 GPGRELIYNQKEGHFPRVTTVSDLTKRNNMDFSIRISNITPADAGTYYCVKFRKGSPDHV 131

Qy        194 EFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 253
              |||       |     |     : | :: ||:    |           |   ||      |
Db        132 EFK-----SGAGTELSVRAKPSAP-VVSGPAARATP---------QHTVSFTCESHGFSP 176

Qy        254 EDPEVKFNWYVDGVEVHNAKTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
              |  :   |: :| |: : :|    |  :       :|| :||     :|   :      |:
Db        177 RD--ITLKWFKNGNELSDFQTNVDPAGDSVSYSIHSTAKVVLTREDVHSQVI------CE 228

Qy        308 VSNKALPA-PIEKT--ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 364
              |::  |   |:  |  :|:    |   :| |  | | |   |||::|| |: |||  : :
Db        229 VAHVTLQGDPLRGTANLSETIRVPPTLEV-TQQPVRAE---NQVNVTCQVRKFYPQRLQL 284

Qy        365 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK 424
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Db        285 TWLENGNVSRTETASTLTENKDGTYNWMSWLLVNVSAHRDDVKLTCQVEHDG------QP 338

Qy        425 SLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTASALPDPPAA 484

Db        339 AVSKSHDLKV--------------------------------SAHPKEQGSNTAPGPALA 366

Qy        485 SALPAALAVISFLLG----LGLGVACV 507

Db        367 SAAP---LLIAFLLGPKVLLVVGVSVI 390


RESULT 94
Q8NFP4
ID   Q8NFP4      PRELIMINARY;      PRT;   955 AA.
AC   Q8NFP4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Glycosyl-phosphatidyl-inositol-MAM.
GN   GPIM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22077705; PubMed=12082541;
RA   De Juan C., Iniesta P., Gonzalez-Quevedo R., Moran A.,
RA   Sanchez-Pernaute A., Torres A.J., Balibrea J.L., Diaz-Rubio E.,
RA   Cruces J., Benito M.;
RT   "Genomic organization of a novel glycosylphosphatidylinositol MAM gene
RT   expressed in human tissues and tumors.";
RL   Oncogene 21:3089-3094(2002).
CC   -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR   EMBL; AF478693; AAM77220.1; -.
DR   Genew; HGNC:19267; MDGA1.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016163; F:nitrogenase activity; IEA.
DR   GO; GO:0009399; P:nitrogen fixation; IEA.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000998; MAM_domain.
DR   InterPro; IPR000318; Nitrognse_comp1.
DR   Pfam; PF00047; ig; 6.
DR   Pfam; PF00629; MAM; 1.
DR   PRINTS; PR00020; MAMDOMAIN.
DR   SMART; SM00409; IG; 6.
DR   SMART; SM00408; IGc2; 6.
DR   SMART; SM00137; MAM; 1.
DR   PROSITE; PS50835; IG_LIKE; 6.
DR   PROSITE; PS50060; MAM_2; 1.
DR   PROSITE; PS00699; NITROGENASE_1_1; 1.
KW   Glycoprotein; Immunoglobulin domain.
SQ   SEQUENCE   955 AA;  105790 MW;  BD41A1EB10A05962 CRC64;

  Query Match             6.7%;  Score 181.5;  DB 4;  Length 955;
  Best Local Similarity   21.8%;  Pred. No. 6.2e-06;
  Matches   99;  Conservative   55;  Mismatches  151;  Indels  149;  Gaps   18;

Qy         36 TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLI 95

Db        152 TVFLRCTVNSNPPARFIWKRGSD-----------TLSHSQDNG-VDIYEPLYTQGETKVL 199

Qy         96 -IKNLKIEDSDTYICEVEDQKE---EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151

Db        200 KLKNLRPQDYASYTCQVSVRNVCGIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENV 258

Qy        152 SVQC-----------------RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN---- 189

Db        259 TVQCLLTGGDPLPQLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGYYNCTATNNVGNP 317


Qy        190 ----------QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMI 238

Db        318 AKKTVNLLVRSMKNATFQI-----------------TPDVI----------KESENIQL 349

Qy        239 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 298

Db        350 GQDLKLSCHVDAVPQE--KVTYQWFKNGKPARMSKRLLVTRNDPELPAVTSSLELIDLHF 407

Qy        299 LNGKEYKCKVSNKALPAP---IEKTISKAKGQPREPQVYTLPPSRDELTKNQVS---LTC 352

Db        408 SDYGTYLCMASPPGAPVPDLSVEVNIS----SETVPPTISVPKGRAVVTVREGSPAELQC 463

Qy        353 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412

Db        464 EVRG--------------------KPRPPVLWS----------RVDK------------ 480

Qy        413 MHEALHNHYTQKSLSLSPGLQLDETCAEAQDGEL 446

Db        481 ----------EAALLPSGLPLEET----PDGKL 499


RESULT 95
Q8BLX5
ID   Q8BLX5      PRELIMINARY;      PRT;   379 AA.
AC   Q8BLX5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Weakly similar to signal-regulatory protein beta-1 precursor.
GN   9930027N05RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK040982; BAC30768.1; -.
DR   MGD; MGI:2444824; 9930027N05Rik.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
SQ   SEQUENCE   379 AA;  42409 MW;  055BAE20759CF6D5 CRC64;

  Query Match             6.7%;  Score 181;  DB 11;  Length 379;
  Best Local Similarity   20.1%;  Pred. No. 1.9e-06;
  Matches   88;  Conservative   70;  Mismatches  155;  Indels  124;  Gaps   17;

Qy          5 VPFRHLLLVLQLALLPAATQGNKVVLGKK------GDTVELTCTASQKKSI----QFHWK 54

Db         10 IPHCVLLLILLLGLKGAAVRELKVIQPVKSPFVGAGGSATLNCTVTYLLPVGPIKWYRGV 69

Qy         55 NSNQIKILGNQGSFLTKGPSKLNDRAD-SRRSLWDQGNFPLIIKNLKIEDSDTYICEVED 113

Db         70 GQSRLLIYPFTGEYF----PRITSVSDVKKRSNLD---FSIRISNVTPADSGTYYC-VKF 121

Qy        114 QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQ 173

Db        122 QRG---------SSEPDIEIQSGGGTELSVFAKP-SSPMVS--GPAARAVP--------- 160

Qy        174 LELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK 233
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```
Db        161 ---QQTVTFTC--------------------------RSHG-----------FFP---- 175

Qy        234 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 293
                                      :   |: :| |: : :|    |: : :||| | : |
Db        176 ----------------------QNLTLKWFKNGNEISHLETSVEPEETSVSYRVSSTVQV 213

Qy        294 LHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPS-----RDELTKNQ 347
              : :      :  |:| :  |  ||:       :|     ::  :||:     : :  |
Db        214 VLEPRDVRSQIICEVDHVTLDRAPL-------RGIAHISEIIQVPPTLEISQQPTMVWNV 266

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              :::|| :: |||    | |  ||          ::: ||::  | | |: |  ::  |
Db        267 INVTCQIQKFYPRRFQVTWLENGNISRREVPFTHIVNKDGTYNWISWLLVNISALEENMV 326

Qy        408 FSCSVMH----EALHNH 420
               :| | |    | :  |
Db        327 VTCQVEHDGQAEVIETH 343


RESULT 96
Q8BFX8
ID   Q8BFX8      PRELIMINARY;      PRT;   397 AA.
AC   Q8BFX8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Weakly similar to signal-regulatory protein beta-1 precursor.
GN   9930027N05RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK036935; BAC29645.1; -.
DR   EMBL; AK054545; BAC35818.1; -.
DR   MGD; MGI:2444824; 9930027N05Rik.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
SQ   SEQUENCE   397 AA;  44157 MW;  E1DE9DFAAC83D676 CRC64;

  Query Match             6.7%;  Score 181;  DB 11;  Length 397;
  Best Local Similarity   20.1%;  Pred. No. 2e-06;
  Matches   88;  Conservative   70;  Mismatches  155;  Indels  124;  Gaps   17;

Qy          5 VPFRHLLLVLQLALLPAATQGNKVVLGKK------GDTVELTCTASQKKSI----QFHWK 54
              :|   |||:| | |  || :  ||:   |      | :  | ||  :    :     :
Db         10 IPHCVLLLIILLGLKGAAVRELKVIQPVKSFFVGAGGSATLNCTVTYLLPVGPIKWYRGV 69

Qy         55 NSNQIKILGNQGSFLTKGPSKLNDRAD-SRRSLWDQGNFPLIIKNLKIEDSDTYICEVED 113
               ::: |   | :       ::   :|  :||  |   | : | |:   || || | |:
Db         70 GQSRLLIYPFTGEYF----PRITSVSDVKKRSNLD---FSIRISNVTPADSGTYYC-VKF 121

Qy        114 QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQ 173
              |:          ::  |  :  |    |:: : | ||| |    |  : :
Db        122 QRG---------SSEPDIEIQSGGGTELSVFAKP-SSPMVS--GPAARAVP--------- 160

Qy        174 LELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK 233
                | : |:||                ::|              ||
Db        161 ---QQTVTFTC--------------------------RSHG-----------FFP---- 175

Qy        234 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 293
                                      :   |: :| |: : :|    |: : :||| | : |
Db        176 ----------------------QNLTLKWFKNGNEISHLETSVEPEETSVSYRVSSTVQV 213

Qy        294 LHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPS-----RDELTKNQ 347
              : :      :  |:| :  |  ||:       :|     ::  :||:     : :  |
Db        214 VLEPRDVRSQIICEVDHVTLDRAPL-------RGIAHISEIIQVPPTLEISQQPTMVWNV 266

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 407
              :::|| :: |||    | |  ||          ::: ||::  | | |: |  ::  |
Db        267 INVTCQIQKFYPRRFQVTWLENGNISRREVPFTHIVNKDGTYNWISWLLVNISALEENMV 326

Qy        408 FSCSVMH----EALHNH 420
               :| | |    | :  |
Db        327 VTCQVEHDGQAEVIETH 343


RESULT 97
Q96I69
ID   Q96I69      PRELIMINARY;      PRT;   233 AA.
AC   Q96I69;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC007782; AAH07782.1; -.
DR   PIR; S12440; S12440.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004812; F:tRNA ligase activity; IEA.
DR   GO; GO:0006418; P:amino acid activation; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;  24802 MW;  C694F8397B27650B CRC64;

  Query Match             6.5%;  Score 176.5;  DB 4;  Length 233;
  Best Local Similarity   26.5%;  Pred. No. 2.2e-06;
  Matches   50;  Conservative   35;  Mismatches   87;  Indels   17;  Gaps    6;

Qy        240 RTPEVTCVVVDVSHEDPEVKFNWY------VDGVEVHNAKTKPR---EEQYNSTYRVVSV 290
              :|  :||   ::  :     |||         : |:  | :|    |    |    :
Db         35 QTARITCGGSNLGSK----SVNWYQLRPGQAPILVVYENKERPAGIPERLSALTSEETAT 90

Qy        291 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK--GQPR-EPQVYTLPPSRDELTKNQ 347
              ||:      :  :| |:| :      :  | ::    |||:  | |   ||| :||  |:
Db         91 LTISSVVAGDEADYFCQVWDTTSQQYVFGTGTQVTVLGQPKANPTVTLFPPSSEELQANK 150

Qy        348 VSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 406
              :| ||:  |||  : | |:::| | :   :|| |    |:  :   | ||::   :|:
Db        151 ATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHR 210

Qy        407 VFSCSVMHE 415
               :|| | ||
Db        211 SYSCQVTHE 219


RESULT 98
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```
Q90530
ID   Q90530      PRELIMINARY;      PRT;   259 AA.
AC   Q90530;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Novel antigen receptor (Fragment).
OS   Ginglymostoma cirratum (Nurse shark).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC   Ginglymostomatidae; Ginglymostoma.
OX   NCBI_TaxID=7801;
RN   [1]
RP   SEQUENCE OF 1-235 FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=95183140; PubMed=7877689;
RA   Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA   Flajnik M.F.;
RT   "A new antigen receptor gene family that undergoes rearrangement and
RT   extensive somatic diversification in sharks.";
RL   Nature 374:168-173(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Greenberg A.S.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U18687; AAB48358.1; -.
DR   HSSP; P01842; 7FAB.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Receptor.
FT   NON_TER    259    259
SQ   SEQUENCE   259 AA;  28245 MW;  07F9860A92318B6E CRC64;

  Query Match             6.5%;  Score 176.5;  DB 13;  Length 259;
  Best Local Similarity   24.2%;  Pred. No. 2.5e-06;
  Matches   64;  Conservative   34;  Mismatches  103;  Indels   63;  Gaps   11;

Qy        223 PSVFLFPPKPKDTLMISRTPE-----------VTCVVVDVSH----------------ED 255
              | ||         |  : :||             : ||: | |:                |:
Db         14 PYVF--------TARVDQTPRSVTKETGESLTINCVLRDASYALGHTCWFRKKSGSTKEE 65

Qy        256 PEVKFNWYVDGV-EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314
                 ||: |  | |         :   |||     |     :|        |       ||
Db         66 NISPGGRYVETVNSVQNLLINDLTVEDGGTYRCGGSL----YNW-------CSCETDVLP 114

Qy        315 -----APIEKTISKAKGQPREPQVYTL--PPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
                  |    |::   | |  | : :|    : ::     | | ||: |:|| :||| |:
Db        115 YAACGAGTAVTVN--PGIPPSPPIVSLLHSATEEQRANRFVQLVCLISGYYPENIAVSWQ 172

Qy        368 SNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
               | :   : : || ||  |   |   | | |    | :|:|:|| | | |  ::  ::
Db        173 KNTKTITSGFATTSPVKTSSNDFSCASLLKVPLQEWSRGSVYSCQVSHSATSSNQRKEIR 232

Qy        427 SLSPGLQLDETCAEAQDGELDGLW 450
              | |       |     :|  :: :|
Db        233 STS------EIAVLLRDPTVEEIW 250


RESULT 99
Q28260
ID   Q28260      PRELIMINARY;      PRT;   739 AA.
AC   Q28260;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular cell adhesion molecule-1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ballantyne C.M., Clubb F.J., Perrard J.L., Radovencovic B.,
RA   Youker K.A., Smith C.W., Entman M.L., Hawkins H.K., Frazier O.H.,
RA   Willerson J.T.;
RT   "Increased Expression of VCAM-1 and ICAM-1 in Early Cardiac Allograft
RT   Arteriopathy in the Dog.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U32086; AAA84866.1; -.
DR   HSSP; P19320; 1VCA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016337; P:cell-cell adhesion; IEA.
DR   InterPro; IPR003987; ICAM_VCAM-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003989; VCAM-1.
DR   Pfam; PF00047; ig; 7.
DR   PRINTS; PR01472; ICAMVCAM1.
DR   PRINTS; PR01474; VCAM1.
DR   SMART; SM00408; IGc2; 4.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Immunoglobulin domain.
SQ   SEQUENCE   739 AA;  81412 MW;  BB5DA3853739C615 CRC64;

  Query Match             6.5%;  Score 176.5;  DB 6;  Length 739;
  Best Local Similarity   21.9%;  Pred. No. 1.1e-05;
  Matches  111;  Conservative   65;  Mismatches  163;  Indels  167;  Gaps   26;

Qy         32 KKGDTVELTCTASQKKSIQFHWK---NSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD 88
              ::| :| :|| :       |  |    ::  :::|
Db        237 QEGGSVTMTCASEGLPPPQIFWSKKLDNGNLQLL-------------------------- 270

Qy         89 QGNFPLIIKNLKIEDSDTYIC----EVEDQKEEVQLLV----FGLTANSDTHLLQ--GQS 138
               ||  | :  :::|||  ||:|    ||    :||:|:|    | :  :    ::   | |
Db        271 SGNATLTLIAMRLEDSGTYVCEGVNEVGKDGKEVELIVQEKPFTVEISPGPQIIAQIGDS 330

Qy        139 LTLTLESPPGSSPS----VQCRSPRG--KNIQGGK-TLSVSQLELQDSGTWTCTVLQNQK 191
              : ||       |||     |  ||      ::| | ||::| : |::  :: |||    |
Db        331 VVLTCGVTDCESPSFSWRTQIDSPLSGTVKVEGAKSTLTLSPVNLENEHSYLCTVTCGHK 390

Qy        192 KVE--FKIDIVPCPA-------------PEPKSCDKTHTCP------ELLGGPSV---- 225
              |:|   |:|:   |                |   ||:  :  |       ||  | ::
Db        391 KLEKGIKVDLYSFPRDPEVEMSGLLVDGNPVTVSCEVPNVYPSDRLEIELFKGETIIESK 450

Qy        226 -FL---------------------------------------FPPKPK---DTLMISRT 241
               ||                                       | || :    || ::
Db        451 SFLEDMDKKSLETKSLEMTFIPTTEDTGKVLVCLAKLHIDEMEFEPKQRQSTQTLYVNVA 510

Qy        242 PEVTCVVVDVS---HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS---VLTVLH 295
              |  | |||  |    |   |      ||:   |     |    |   : :|   :||:
Db        511 PRDTTVVVSPSSIVEEGSPVNMTCSSDGLPAPNILWSRRLS--NGRLQSLSEDPILTLTS 568

Qy        296 QDWLNGKEYKCKVSNKA--LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ----VS 349
                  :   | |:  |:|      :|  |  |   |:: |:   |    |  |      :|
Db        569 AKMEDSGIYVCEGINQAGISRKEVELIIQVA---PKDIQLIAFP---SESVKEGDTVIIS 622

Qy        350 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS-DGSFFLYSKLTVDKSRWQQGNVF 408
              ||   | |     :     :|   || | ||::      |: | : :   |:
Db        623 CTC---GNVPKTWII-------LKKKAETGDTVLKSRDGAY------TIHKVQLEDAGVY 666

Qy        409 SCSVMHEALHNHYTQKSLSLSPGLQL 434
              |   :||             ||||
Db        667 ECESKNEA-------------GLQL 678


RESULT 100
Q63669
ID   Q63669      PRELIMINARY;      PRT;   739 AA.
AC   Q63669;
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DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular cell adhesion molecule 1 precursor.
GN   VCAM-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague Dawley; TISSUE=Lung;
RX   MEDLINE=92305064; PubMed=1377031;
RA   Williams A.J., Atkins R.C., Fries J.W., Gimbrone M.A.Jr.,
RA   Cybulsky M.I., Collins T.;
RT   "Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.";
RL   Biochim. Biophys. Acta 1131:214-216(1992).
DR   EMBL; X63722; CAA45254.1; -.
DR   HSSP; P19320; 1VCA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016337; P:cell-cell adhesion; IEA.
DR   InterPro; IPR003987; ICAM_VCAM-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003989; VCAM-1.
DR   Pfam; PF00047; ig; 5.
DR   PRINTS; PR01472; ICAMVCAM1.
DR   PRINTS; PR01474; VCAM1.
DR   SMART; SM00408; IGc2; 4.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    739       VASCULAR CELL ADHESION MOLECULE 1.
SQ   SEQUENCE   739 AA;  81136 MW;  A5AAD1172F67FB96 CRC64;

  Query Match             6.5%;  Score 176.5;  DB 11;  Length 739;
  Best Local Similarity   21.4%;  Pred. No. 1.1e-05;
  Matches  101;  Conservative   71;  Mismatches  169;  Indels  131;  Gaps   23;

Qy         33 KGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF 92
              :|  | :|| :    : :  |                |  |  :|            ||
Db        238 EGAAVTMTCASEGLPAPEIFWSKK-----------LDNGVLQLL----------SGNA 274

Qy         93 PLIIKNLKIEDSDTYICE----VEDQKEEVQLLV------FGLTANSDTHLLQGQSLTLT 142
               | :  :::|||  |:||    |   | ||:|:|        ::  |     | |: ||
Db        275 TLTLIAMRMEDSGIYVCEGVNLVGRDKTEVELIVQEKPFTVDISPGSQVAAQVGDSVVLT 334

Qy        143 LESPPGSSPSVQCRSPRGKNIQG-------GKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
               :    |||   |:     : |         ||:| : ::|  :: |||   ::|:|
Db        335 CAAVGCDSPSFSWRTQTDSPLNGEVRDEGATSTLTLSPVGVEDEHSYLCTVTCQRRKLEK 394

Qy        196 KIDIVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV--- 251
              | :     ||           ||: : ||            |:  |   | | | :|
Db        395 TIQVEVYSFPED---------PEIEISGP-----------LVHGRPVTVNCTVPNVYPF 433

Qy        252 SHEDPEV---------KFNWYVDGVEVHNAKTKPREEQY----NSTYRVVSVLTVLHQDW 298
              | : |:          ||    : :   : :||  | :       | : :  |  ||
Db        434 DHLEIELLKGETTLLNKF--LREEIGTKSLETKSLEMTFIPTAEDTGKALVCLAKLHSSQ 491

Qy        299 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP-PSRDELTKNQVSLTCLVKGF 357
              :   | | : | : |   :           |:|| ::  | |  :|   : |:|||   ||
Db        492 ME-SEPKQRQSTQTLYVNV---------APKEPTIWVSPSPVPEE--GSPVNLTCSSDGF 539

Qy        358 YPSDIAVEWE---SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH 414
                  |    |     ||: :       |:  :    |: :|:       :   :: |  ::
Db        540 PTPKIL--WSRQLKNGELQ-------PLSQNTTLSFMATKM-------EDSGIYVCEGIN 583

Qy        415 EALHNHYTQKSLSL-----SPGLQL-----------DETCAEAQDGELDGLW 450
              ||     ::||: |     |  :||           |     | :  :|
Db        584 EA---GISKKSVELIIQGSSKDIQLTVFPSKSVKEGDTVIISCTCGSVPEIW 632


Search completed: August  3, 2004, 13:13:56
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Job time : 42.157 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 3, 2004, 12:50:44 ; Search time 7.03139 Seconds
(without alignments)
3791.557 Million cell updates/sec

Title: SEQ8
Perfect score: 2702
Sequence: 1 MNRGVPFRHLLLVLQLALLP.....VISFLLGLGLGVACVLARTR 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 125 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1227.5	45.4	330	1	GC1_HUMAN	P01857 homo sapien
2	1133	41.9	290	1	GC3_HUMAN	P01860 homo sapien
3	1130.5	41.8	326	1	GC2_HUMAN	P01859 homo sapien
4	1119	41.4	327	1	GC4_HUMAN	P01861 homo sapien
5	1023	37.9	458	1	CD4_HUMAN	P01730 homo sapien
6	999	37.0	458	1	CD4_PANTR	P16004 pan troglod
7	955.5	35.4	398	1	GC3M_MOUSE	P03987 mus musculu
8	932.5	34.5	393	1	GC1M_MOUSE	P01869 mus musculu
9	916.5	33.9	458	1	CD4_MACFA	P79185 macaca fasc
10	910	33.7	458	1	CD4_MACFU	P79184 macaca fusc
11	906.5	33.5	399	1	GCAM_MOUSE	P01865 mus musculu
12	904	33.5	458	1	CD4_MACMU	P16003 macaca mula
13	903	33.4	458	1	CD4_MACNE	Q08340 macaca neme
14	899	33.3	323	1	GC_RABIT	P01870 oryctolagus
15	894.5	33.1	329	1	GC2_CAVPO	P01862 cavia porce
16	885	32.8	458	1	CD4_CERAE	Q08338 cercopithec
17	877.5	32.5	405	1	GCBM_MOUSE	P01867 mus musculu
18	857.5	31.7	329	1	GC3_MOUSE	P22436 mus musculu
19	833	30.8	333	1	GCB_RAT	P20761 rattus norv
20	823.5	30.5	326	1	GC1_RAT	P20759 rattus norv
21	823	30.5	329	1	GCC_RAT	P20762 rattus norv
22	818.5	30.3	324	1	GC1_MOUSE	P01868 mus musculu
23	805.5	29.8	330	1	GCAA_MOUSE	P01863 mus musculu
24	801	29.6	335	1	GCAB_MOUSE	P01864 mus musculu
25	792.5	29.3	322	1	GCA_RAT	P20760 rattus norv
26	784	29.0	397	1	CD4_CERTO	Q08336 cercocebus
27	783	29.0	397	1	CD4_ERYPA	Q08339 erythrocebu
28	781.5	28.9	336	1	GCB_MOUSE	P01866 mus musculu
29	743	27.5	457	1	CD4_SAISC	Q29037 saimiri sci
30	617.5	22.9	463	1	CD4_CANFA	P33705 canis famil
31	601.5	22.3	459	1	CD4_RABIT	P46630 oryctolagus
32	495	18.3	457	1	CD4_RAT	P05540 rattus norv
33	475	17.6	457	1	CD4_MOUSE	P06332 mus musculu
34	388	14.4	421	1	EPC_MOUSE	P06336 mus musculu
35	384.5	14.2	454	1	MUC_HUMAN	P01871 homo sapien
36	373.5	13.8	476	1	MUCM_MOUSE	P01873 mus musculu
37	370.5	13.7	429	1	EPC_RAT	P01855 rattus norv
38	369.5	13.7	479	1	MUCM_RABIT	P04221 oryctolagus
39	369	13.7	450	1	MUC_CANFA	P01874 canis famil
40	365.5	13.5	391	1	MUCB_HUMAN	P04220 homo sapien
41	362	13.4	455	1	MUC_MOUSE	P01872 mus musculu
42	361.5	13.4	428	1	EPC_HUMAN	P01854 homo sapien
43	360	13.3	458	1	MUC_RABIT	P03988 oryctolagus
44	354.5	13.1	457	1	MUC_SUNMU	P20768 suncus muri
45	344	12.7	454	1	MUC_MESAU	P06337 mesocricetu
46	316.5	11.7	240	1	CD7_HUMAN	P09564 homo sapien
47	312	11.5	438	1	HVC2_HETFR	P23085 heterodontu
48	310.5	11.5	446	1	MUC_CHICK	P01875 gallus gall
49	301.5	11.2	461	1	HVCM_HETFR	P23088 heterodontu
50	294.5	10.9	340	1	ALC2_HUMAN	P01877 homo sapien
51	294	10.9	438	1	HVCS_HETFR	P23087 heterodontu
52	293	10.8	299	1	ALC_RABIT	P01879 oryctolagus
53	286.5	10.6	370	1	HVC1_HETFR	P23084 heterodontu
54	281	10.4	393	1	HVC3_HETFR	P23086 heterodontu
55	279	10.3	353	1	ALC1_GORGO	P20758 gorilla gor
56	277.5	10.3	353	1	ALC1_HUMAN	P01876 homo sapien
57	276.5	10.2	481	1	MUCM_ICTPU	P23735 ictalurus p
58	264.5	9.8	344	1	ALC_MOUSE	P01878 mus musculu
59	199	7.4	513	1	SHS1_MOUSE	P97797 m protein-t
60	192	7.1	509	1	SHS1_RAT	P97710 r protein-t
61	188.5	7.0	387	1	SRB2_HUMAN	Q9p1w8 homo sapien
62	188.5	7.0	506	1	SHS1_BOVIN	O46631 bos taurus
63	177.5	6.6	105	1	LAC1_MOUSE	P01843 mus musculu
64	176.5	6.5	739	1	VCA1_RAT	P29534 rattus norv
65	175.5	6.5	4391	1	PGBM_HUMAN	P98160 homo sapien
66	172	6.4	104	1	LAC2_RAT	P20767 rattus norv
67	170	6.3	383	1	DTC_HUMAN	P01880 homo sapien
68	167	6.2	847	1	CD22_HUMAN	P20273 homo sapien
69	166.5	6.2	398	1	SRB1_HUMAN	O00241 homo sapien
70	164	6.1	6632	1	UN89_CAEEL	O01761 caenorhabdi
71	163	6.0	104	1	LAC3_MOUSE	P01845 mus musculu
72	163	6.0	3707	1	PGBM_MOUSE	Q05793 mus musculu
73	162.5	6.0	213	1	ILL1_HUMAN	P15814 homo sapien
74	161	6.0	104	1	LAC2_MOUSE	P01844 mus musculu
75	161	6.0	258	1	HB2D_PIG	P15983 sus scrofa
76	160.5	5.9	739	1	VCA1_HUMAN	P19320 homo sapien
77	160	5.9	1197	1	CAM1_BRARE	Q90478 brachydanio
78	159	5.9	105	1	LAC_HUMAN	P01842 homo sapien
79	156.5	5.8	503	1	SHS1_HUMAN	P78324 h protein-t
80	156	5.8	105	1	LAC_PIG	P01846 sus scrofa
81	153.5	5.7	105	1	LAC5_MUSSP	P20765 mus spretus
82	153	5.7	105	1	LAC_RABIT	P01847 oryctolagus
83	153	5.7	106	1	KACB_RABIT	P01839 oryctolagus
84	151.5	5.6	702	1	CEA5_HUMAN	P06731 homo sapien
85	150	5.6	106	1	KACA_RAT	P01836 rattus norv
86	149.5	5.5	261	1	HB2C_PIG	P15982 sus scrofa
87	149	5.5	348	1	KILO_RAT	Q9z0j8 rattus norv
88	148	5.5	106	1	KAC_HUMAN	P01834 homo sapien
89	148	5.5	1369	1	NFAS_CHICK	O42414 gallus gall
90	147	5.4	338	1	LAMP_HUMAN	Q13449 homo sapien
91	147	5.4	1240	1	NFAS_MOUSE	Q810u3 mus musculu
92	147	5.4	1242	1	NPHN_MOUSE	Q9qzs7 mus musculu
93	146	5.4	104	1	LAC1_RAT	P20766 rattus norv
94	146	5.4	1259	1	CAML_RAT	Q05695 rattus norv
95	145.5	5.4	103	1	LAC_CHICK	P20763 gallus gall
96	145	5.4	106	1	KACB_RAT	P01835 rattus norv
97	144.5	5.3	333	1	AMAL_DROME	P15364 drosophila
98	144.5	5.3	739	1	VCA1_MOUSE	P29533 mus musculu
99	144	5.3	338	1	LAMP_RAT	Q62813 rattus norv
100	143.5	5.3	1240	1	NFAS_RAT	P97685 rattus norv
101	143	5.3	106	1	KAC_MOUSE	P01837 mus musculu
102	143	5.3	1260	1	CAML_MOUSE	P11627 mus musculu
103	142.5	5.3	761	1	NCA2_HUMAN	P13592 homo sapien
104	142.5	5.3	773	1	PIGR_RABIT	P01832 oryctolagus
105	142.5	5.3	1240	1	NFAS_HUMAN	O94856 homo sapien
106	140.5	5.2	1266	1	NGCA_CHICK	Q03696 gallus gall

107	140	5.2	268	1	HB2X_HUMAN	P05538 homo sapien
108	140	5.2	273	1	2DOB_HUMAN	P13765 homo sapien
109	139	5.1	273	1	2DOB_PANTR	P18467 pan troglod
110	138	5.1	1234	1	NPHN_RAT	Q9r044 rattus norv
111	136	5.0	999	1	MERK_HUMAN	Q12866 homo sapien
112	136	5.0	2012	1	DSCA_HUMAN	O60469 homo sapien
113	135.5	5.0	105	1	LAC5_MOUSE	P20764 mus musculu
114	135	5.0	837	1	NCM2_MOUSE	O35136 mus musculu
115	134.5	5.0	261	1	HB22_HUMAN	P01919 homo sapien
116	134.5	5.0	261	1	HB24_HUMAN	P01920 homo sapien
117	134.5	5.0	853	1	NCA1_BOVIN	P31836 bos taurus
118	133.5	4.9	858	1	NCA1_RAT	P13596 rattus norv
119	133.5	4.9	1694	1	SN_MOUSE	Q62230 mus musculu
120	132.5	4.9	261	1	HB21_HUMAN	P01918 homo sapien
121	132	4.9	231	1	HB2L_CHICK	P23068 gallus gall
122	132	4.9	1277	1	CAML_FUGRU	Q98902 fugu rubrip
123	132	4.9	1302	1	NRG_DROME	P20241 drosophila
124	131.5	4.9	202	1	DTC_RAT	P01883 rattus norv
125	131.5	4.9	345	1	OPCM_BOVIN	P11834 bos taurus

ALIGNMENTS

```
RESULT 1
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;      PRT;   330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of
CC       35, 116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   PDB; 1AJ7; 12-NOV-97.
DR   PDB; 1D5B; 09-FEB-00.
DR   PDB; 1D5I; 09-FEB-00.
DR   PDB; 1D6V; 04-OCT-00.
DR   PDB; 1DN2; 17-MAY-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FCC; 20-JUL-95.
DR   PDB; 1HZH; 12-JUN-02.
DR   PDB; 1I7Z; 08-AUG-01.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   PDB; 1L6X; 10-APR-02.
DR   PDB; 2RCS; 12-NOV-97.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
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DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    147
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    166
FT   TURN        168    171
FT   STRAND      176    179
FT   TURN        180    181
FT   STRAND      182    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      260    265
FT   STRAND      270    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      305    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    325
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             45.4%;  Score 1227.5;  DB 1;  Length 330;
  Best Local Similarity   74.5%;  Pred. No. 1.6e-71;
  Matches  246;  Conservative    7;  Mismatches   22;  Indels   55;  Gaps    6;

Qy        151 PSVQCRSPRGKNIQGG-------------KTLSVS-------------QLELQDSG---- 180
              |||   :|  |:  ||              : ::||               || ||
Db          6 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 65

Qy        181 --------------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLG 221
                           |: | |  | |    |:|      ||||||||||     |||||
Db         66 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG 119

Qy        222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 179

Qy        282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 239

Qy        342 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 299

Qy        402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              ||||||||||||||||||||||||||||||
Db        300 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 329


RESULT 2
GC3_HUMAN
ID   GC3_HUMAN      STANDARD;      PRT;   290 AA.
AC   P01860;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN   IGHG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (DISEASE PROTEIN WIS).
RX   MEDLINE=81021548; PubMed=6774747;
RA   Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT   "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT   gamma 3 heavy-chain disease protein Wis.";
RL   Biochemistry 19:4304-4308(1980).
RN   [2]
RP   REVISIONS TO 12-97 (PROTEIN WIS).
RX   MEDLINE=77118561; PubMed=402363;
RA   Michaelsen T.E., Frangione B., Franklin E.C.;
RT   "Primary structure of the 'hinge' region of human IgG3. Probable
RT   quadruplication of a 15-amino acid residue basic unit.";
RL   J. Biol. Chem. 252:883-889(1977).
RN   [3]
RP   REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX   MEDLINE=77021516; PubMed=823945;
RA   Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT   "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT   Structure of the Fc fragment of immunoglobulin G3.";
RL   Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN   [4]
RP   SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX   MEDLINE=82247835; PubMed=6808505;
RA   Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA   Franklin E.C., Hood L., Buxbaum J.N.;
RT   "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT   gene deletion model.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC   -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC       interchain disulfide bond at position 7 in addition to the 11
CC       normally present in the hinge region.
CC   -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC   -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
CC       Ref.2.
CC   -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC       and all of the CH1 region.
CC   -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC       of the CH1 region, and part of the hinge compared with normal
CC       gamma-3 heavy chains.
CC   -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC       or another gamma chain subclass.
CC   -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC       times as long as in other gamma chains and contains three
CC       identical 15-residue segments preceded by a similar 17-residue
CC       segment (12-28).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; J00231; AAA52805.1; ALT_SEQ.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5527; IGHG3.
DR   MIM; 147120; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN       12     73       HINGE.
FT   DOMAIN       74    183       CH2.
FT   DOMAIN      184    289       CH3.
FT   REPEAT       29     43
FT   REPEAT       44     58
FT   REPEAT       59     73
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .).
FT   DISULFID      7      7       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     24     24       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     27     27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     33     33       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     39     39       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     42     42       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     48     48       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     54     54       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     57     57       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     63     63       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     69     69       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID     72     72       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .).
FT   MOD_RES     290    290       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT     126    127       QV -> EB (IN ZUC).
FT                                /FTId=VAR_003890.
FT   VARIANT     134    134       P -> L (IN OMM).
FT                                /FTId=VAR_003891.
FT   VARIANT     139    139       F -> Y (IN OMM).
FT                                /FTId=VAR_003892.
FT   VARIANT     182    182       T -> A (IN OMM).
FT                                /FTId=VAR_003893.
FT   VARIANT     227    227       S -> N (IN OMM).
FT                                /FTId=VAR_003894.
FT   VARIANT     227    227       MISSING (IN ZUC).
FT                                /FTId=VAR_003895.
FT   VARIANT     279    279       F -> Y (IN OMM).
FT                                /FTId=VAR_003896.
SQ   SEQUENCE   290 AA;  32331 MW;  E69CBC95705B2F46 CRC64;

  Query Match             41.9%;  Score 1133;  DB 1;  Length 290;
  Best Local Similarity   88.2%;  Pred. No. 1.5e-65;
  Matches  209;  Conservative   13;  Mismatches    9;  Indels    6;  Gaps    2;

Qy        201 PCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 254
              |||  |||||||    |     |||||||||||||||||||||||||||||||||||||
Db         53 PCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 112

Qy        255 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314
              ||||:| ||||||:||||||||||:|:|||:||||||||||||:||:|||||||||||||
Db        113 DPEVQFKWYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALP 172

Qy        315 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
              ||||||||| |||||||||||||||:|:|||||||||||||||||||||||||:|||||
Db        173 APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPEN 232

Qy        375 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
              || ||||:|||||||||||||||||||||:|||||||||||| :||||||||||
Db        233 NYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG 289


RESULT 3
GC2_HUMAN
ID   GC2_HUMAN      STANDARD;      PRT;   326 AA.
AC   P01859;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   IGHG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197621; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma
RT   heavy chain constant region genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
RX   MEDLINE=80114419; PubMed=118920;
RA   Hofmann T., Parr D.M.;
RT   "A note of the amino acid sequence of residues 381-391 of human
RT   immunoglobulins gamma chains.";
RL   Mol. Immunol. 16:923-925(1979).
RN   [7]
RP   REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA   Hofmann T., Parr D.M.;
RL   Submitted (MAR-1980) to the PIR data bank.
RN   [8]
RP   SEQUENCE OF 1-121 (DOT).
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RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=72033500; PubMed=4940472;
RA   Milstein C., Frangione B.;
RT   "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL   Biochem. J. 121:217-225(1971).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=69064124; PubMed=5782707;
RA   Frangione B., Milstein C., Pink J.R.L.;
RT   "Structural studies of immunoglobulin G.";
RL   Nature 221:145-148(1969).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00230; AAB59393.1; -.
DR   PIR; A93906; G2HU.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5526; IGHG2.
DR   MIM; 147110; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    219       CH2.
FT   DOMAIN      220    326       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    102    102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    103    103       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    140    200
FT   DISULFID    246    304
FT   SITE        156    156       AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT   MOD_RES     326    326       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT      60     60       S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT                                /FTId=VAR_003889.
FT   CONFLICT    109    109       C -> S (IN REF. 3).
SQ   SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;

  Query Match             41.8%;  Score 1130.5;  DB 1;  Length 326;
  Best Local Similarity   82.6%;  Pred. No. 2.5e-65;
  Matches  214;  Conservative   12;  Mismatches   12;  Indels   21;  Gaps    3;

Qy        181 TWTCTV------LQNQKKVEFK--IDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKP 232
              |:|| |       :  | || |  ::  |||||             : ||||||||||
Db         80 TYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPP------------VAGPSVFLFPPKP 126

Qy        233 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 292
              |||||||||||||||||||||||||:||||||||||||||||:|||:||||||||
Db        127 KDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLT 186

Qy        293 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 352
              |:||||||||||||||| |||||||||| |||||||||||||||:|:|||||||||
Db        187 VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC 246

Qy        353 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 412
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        247 LVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 306

Qy        413 MHEALHNHYTQKSLSLSPG 431
              |||||||||||||||||||
Db        307 MHEALHNHYTQKSLSLSPG 325


RESULT 4
GC4_HUMAN
ID   GC4_HUMAN      STANDARD;      PRT;   327 AA.
AC   P01861;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-4 chain C region.
GN   IGHG4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83157104; PubMed=6299662;
RA   Ellison J.W., Buxbaum J.N., Hood L.E.;
RT   "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL   DNA 1:11-18(1981).
RN   [2]
RP   SEQUENCE OF 1-30 AND 81-326.
RX   MEDLINE=70207560; PubMed=4192699;
RA   Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT   "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT   constant region of a gamma 4 chain.";
RL   Biochem. J. 117:33-47(1970).
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K01316; AAB59394.1; ALT_INIT.
DR   PIR; A90933; G4HU.
DR   PDB; 1ADQ; 16-SEP-98.
DR   Genew; HGNC:5528; IGHG4.
DR   MIM; 147130; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    220       CH2.
FT   DOMAIN      221    327       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
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FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    141    201
FT   DISULFID    247    305
SQ   SEQUENCE   327 AA;  35940 MW;  3EDBD811EF208E7A CRC64;

  Query Match             41.4%;  Score 1119;  DB 1;  Length 327;
  Best Local Similarity   83.7%;  Pred. No. 1.3e-64;
  Matches  215;  Conservative   11;  Mismatches   15;  Indels   16;  Gaps    4;

Qy        181 TWTCTV------LQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKD 234
              |:|| |       :  |:|| |    |||     ||      || ||||||||||||||
Db         80 TYTCNVDHKPSNTKVDKRVESKYG-PPCP-----SC----PAPEFLGGPSVFLFPPKPKD 129

Qy        235 TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL 294
              |||||||||||||||||| |||||:|||||||||||||||||||:|||||||||||||
Db        130 TLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVL 189

Qy        295 HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV 354
              |||||||||||||||| ||: |||||||||||||||||||::|:||||||||||||
Db        190 HQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLV 249

Qy        355 KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH 414
              ||||||||||||||||||||||||||||||||||||||:|||||||:||||||||||
Db        250 KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH 309

Qy        415 EALHNHYTQKSLSLSPG 431
              ||||||||||||||| |
Db        310 EALHNHYTQKSLSLSLG 326


RESULT 5
CD4_HUMAN
ID   CD4_HUMAN      STANDARD;      PRT;   458 AA.
AC   P01730;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3).
GN   CD4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85254948; PubMed=2990730;
RA   Maddon P.J., Littman D.R., Godfrey M., Maddon D.E., Chess L.,
RA   Axel R.;
RT   "The isolation and nucleotide sequence of a cDNA encoding the T cell
RT   surface protein T4: a new member of the immunoglobulin gene family.";
RL   Cell 42:93-104(1985).
RN   [2]
RP   REVISION TO 26.
RX   MEDLINE=89028665; PubMed=3263213;
RA   Littman D.R., Maddon P.J., Axel R.;
RT   "Corrected CD4 sequence.";
RL   Cell 55:541-541(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96303695; PubMed=8723724;
RA   Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
RA   Malley T., Gibbs R.A.;
RT   "A gene-rich cluster between the CD4 and triosephosphate isomerase
RT   genes at human chromosome 12p13.";
RL   Genome Res. 6:314-326(1996).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT TRP-265.
RX   MEDLINE=91216786; PubMed=1708753;
RA   Hodge T.W., Sasso D.R., McDougal J.S.;
RT   "Humans with OKT4-epitope deficiency have a single nucleotide base
RT   change in the CD4 gene, resulting in substitution of TRP240 for
RT   ARG240.";
RL   Hum. Immunol. 30:99-104(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 28-424 FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=93049640; PubMed=1425921;
RA   Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT   "Cloning and sequences of primate CD4 molecules: diversity of the
RT   cellular receptor for simian immunodeficiency virus/human
RT   immunodeficiency virus.";
RL   Eur. J. Immunol. 22:2973-2981(1992).
RN   [7]
RP   SEQUENCE OF 26-394.
RX   MEDLINE=90078232; PubMed=2592374;
RA   Carr S.A., Hemling M.E., Folena-Wasserman G., Sweet R.W., Anumula K.,
RA   Barr J.R., Huddleston M.J., Taylor P.;
RT   "Protein and carbohydrate structural analysis of a recombinant
RT   soluble CD4 receptor by mass spectrometry.";
RL   J. Biol. Chem. 264:21286-21295(1989).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 26-208.
RX   MEDLINE=91061881; PubMed=1701030;
RA   Wang J., Yan Y., Garrett T.P., Liu J., Rodgers D.W., Garlick R.L.,
RA   Tarr G.E., Husain Y., Reinherz E.L., Harrison S.C.;
RT   "Atomic structure of a fragment of human CD4 containing two
RT   immunoglobulin-like domains.";
RL   Nature 348:411-418(1990).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-208.
RX   MEDLINE=91061882; PubMed=2247146;
RA   Ryu S.-E., Kwong P.D., Truneh A., Porter T.G., Arthos J.,
RA   Rosenberg M., Dai X., Xuong N.-H., Axel R., Sweet R.W.,
RA   Hendrickson W.A.;
RT   "Crystal structure of an HIV-binding recombinant fragment of human
RT   CD4.";
RL   Nature 348:419-426(1990).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS) OF 26-388.
RX   MEDLINE=97311402; PubMed=9168119;
RA   Wu H., Kwong P.D., Hendrickson W.A.;
RT   "Dimeric association and segmental variability in the structure of
RT   human CD4.";
RL   Nature 387:527-530(1997).
RN   [11]
RP   PALMITOYLATION.
RX   MEDLINE=92317088; PubMed=1618861;
RA   Crise B., Rose J.K.;
RT   "Identification of palmitoylation sites on CD4, the human
RT   immunodeficiency virus receptor.";
RL   J. Biol. Chem. 267:13593-13597(1992).
```

```
CC   -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC       receptor interaction. May regulate T-cell activation.
CC   -!- SUBUNIT: Associates with p56-lck.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD4 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd4.htm".
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M12807; AAA35572.1; -.
DR   EMBL; U47924; AAB51309.1; -.
DR   EMBL; M35160; AAA16069.1; -.
DR   EMBL; BC025782; AAH25782.1; -.
DR   PIR; A90872; RWHUT4.
DR   PDB; 1CDH; 30-APR-94.
DR   PDB; 1CDI; 30-APR-94.
DR   PDB; 3CD4; 31-OCT-93.
DR   PDB; 1CDJ; 01-APR-97.
DR   PDB; 1CDU; 01-APR-97.
DR   PDB; 1CDY; 01-APR-97.
DR   PDB; 1WBR; 12-MAR-97.
DR   PDB; 1WIO; 07-JUL-97.
DR   PDB; 1WIP; 07-JUL-97.
DR   PDB; 1WIQ; 07-JUL-97.
DR   PDB; 1G9M; 27-DEC-00.
DR   PDB; 1G9N; 27-DEC-00.
DR   PDB; 1GC1; 19-AUG-98.
DR   PDB; 1JL4; 19-SEP-01.
DR   GlycoSuiteDB; P01730; -.
DR   Genew; HGNC:1678; CD4.
DR   MIM; 186940; -.
DR   GO; GO:0042101; C:T-cell receptor complex; NAS.
DR   GO; GO:0015026; F:coreceptor activity; NAS.
DR   GO; GO:0015029; F:internalization receptor activity; TAS.
DR   GO; GO:0042289; F:MHC class II protein binding; NAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0009405; P:pathogenesis; TAS.
DR   GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; NAS.
DR   GO; GO:0030217; P:T-cell differentiation; NAS.
DR   GO; GO:0045058; P:T-cell selection; NAS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Immune response; Repeat; Signal; Lipoprotein; Palmitate; 3D-structure;
KW   Polymorphism.
FT   SIGNAL       1     25
FT   CHAIN       26    458       T-CELL SURFACE GLYCOPROTEIN CD4.
FT   DOMAIN      26    396       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   397    418       POTENTIAL.
FT   DOMAIN     419    458       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      26    125       IG-LIKE V-TYPE.
FT   DOMAIN     126    203       IG-LIKE C2-TYPE 1.
FT   DOMAIN     204    317       IG-LIKE C2-TYPE 2.
FT   DOMAIN     318    374       IG-LIKE C2-TYPE 3.
FT   CARBOHYD   296    296       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000053.
FT   CARBOHYD   325    325       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000054.
FT   DISULFID    41    109
FT   DISULFID   155    184
FT   DISULFID   328    370       BY SIMILARITY.
FT   LIPID      419    419       S-palmitoyl cysteine.
FT   LIPID      422    422       S-palmitoyl cysteine.
FT   VARIANT    265    265       R -> W (in OKT4-negative populations).
FT                               /FTId=VAR_003906.
FT   STRAND      27     32
FT   TURN        33     34
FT   STRAND      37     39
FT   TURN        44     45
FT   STRAND      51     55
FT   TURN        56     57

  Query Match             37.9%;  Score 1023;  DB 1;  Length 458;
  Best Local Similarity   99.5%;  Pred. No. 2.8e-58;
  Matches  199;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIV 200


RESULT 6
CD4_PANTR
ID   CD4_PANTR      STANDARD;      PRT;   458 AA.
AC   P16004;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3).
GN   CD4.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90182664; PubMed=2107024;
RA   Camerini D., Seed B.;
RT   "A CD4 domain important for HIV-mediated syncytium formation lies
RT   outside the virus binding site.";
RL   Cell 60:747-754(1990).
RN   [2]
RP   SEQUENCE OF 26-424 FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=93049640; PubMed=1425921;
RA   Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT   "Cloning and sequences of primate CD4 molecules: diversity of the
RT   cellular receptor for simian immunodeficiency virus/human
RT   immunodeficiency virus.";
RL   Eur. J. Immunol. 22:2973-2981(1992).
CC   -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC       receptor interaction. May regulate T-cell activation.
CC   -!- SUBUNIT: Associates with p56-lck (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M31135; AAA35407.1; -.
DR   EMBL; X73323; CAA51749.1; -.
DR   PIR; B32722; RWCZT4.
DR   HSSP; P01730; 1WIQ.
DR   GO; GO:0042101; C:T-cell receptor complex; ISS.
DR   GO; GO:0015026; F:coreceptor activity; ISS.
DR   GO; GO:0042289; F:MHC class II protein binding; ISS.
DR   GO; GO:0006955; P:immune response; ISS.
DR   GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR   GO; GO:0030217; P:T-cell differentiation; ISS.
DR   GO; GO:0045058; P:T-cell selection; ISS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Immune response; Repeat; Signal; Lipoprotein; Palmitate.
FT   SIGNAL       1    25       BY SIMILARITY.
FT   CHAIN       26   458       T-CELL SURFACE GLYCOPROTEIN CD4.
FT   DOMAIN      26   396       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   397   418       POTENTIAL.
FT   DOMAIN     419   458       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      26   125       IG-LIKE V-TYPE.
FT   DOMAIN     126   203       IG-LIKE C2-TYPE 1.
FT   DOMAIN     204   317       IG-LIKE C2-TYPE 2.
FT   DOMAIN     318   374       IG-LIKE C2-TYPE 3.
FT   CARBOHYD   296   296       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD   325   325       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID    41   109       BY SIMILARITY.
FT   DISULFID   155   184       BY SIMILARITY.
FT   DISULFID   328   370       BY SIMILARITY.
FT   LIPID      419   419       S-palmitoyl cysteine (By similarity).
FT   LIPID      422   422       S-palmitoyl cysteine (By similarity).
FT   CONFLICT    42    42       T -> N (IN REF. 2).
FT   CONFLICT    62    62       L -> S (IN REF. 2).
FT   CONFLICT   191   191       K -> N (IN REF. 2).
SQ   SEQUENCE   458 AA;  51057 MW;  A7C3AC8A5257D3AD CRC64;

  Query Match             37.0%;  Score 999;  DB 1;  Length 458;
  Best Local Similarity   97.5%;  Pred. No. 9.4e-57;
  Matches  195;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||| |
Db          1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQTK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              |||||||||||||||||| |||||||||| |||||||||||||||||| ||||||||
Db         61 ILGNQGSFLTKGPSKLNDRVDSRRSLWDQGNFTLIIKNLKIEDSDTYICEVGDQKEEVQL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV 200
              ||||||||||||||||||||
Db        181 TWTCTVLQNQKKVEFKIDIV 200


RESULT 7
GC3M_MOUSE
ID   GC3M_MOUSE     STANDARD;      PRT;   398 AA.
AC   P03987;
DT   23-OCT-1986 (Rel. 02, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-3 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
RN   [2]
RP   SEQUENCE OF 328-398 FROM N.A.
RX   MEDLINE=84041483; PubMed=6314258;
RA   Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA   Wall R.;
RT   "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT   segment.";
RL   Nucleic Acids Res. 11:6775-6785(1983).
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00451; AAB59655.1; -.
DR   EMBL; V01526; CAA24767.1; ALT_SEQ.
DR   PIR; A02156; G3MSM.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER      1      1
FT   DOMAIN       1     97       CH1.
FT   DOMAIN      98    113       HINGE.
FT   DOMAIN     114    223       CH2.
FT   DOMAIN     224    327       CH3.
FT   TRANSMEM   346    362       POTENTIAL.
FT   DOMAIN     363    398       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT   333    333       E -> G (IN REF. 2).
FT   CONFLICT   342    342       E -> Q (IN REF. 2).
FT   CONFLICT   388    388       P -> F (IN REF. 2).
SQ   SEQUENCE   398 AA;  43929 MW;  CF7F264B50A41B95 CRC64;

  Query Match             35.4%;  Score 955.5;  DB 1;  Length 398;
  Best Local Similarity   61.4%;  Pred. No. 4.7e-54;
  Matches  180;  Conservative   40;  Mismatches   58;  Indels   15;  Gaps    4;

Qy        170 SVSQLELQDSGTW-----TCTVLQNQKKVEFKIDI---VPCPAPEPKSCDKTHTCP--EL 219
              |:| |    | ||      | |     | |     |   :| |:  | |     :||   :
Db         62 SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----SCPPGNI 116

Qy        220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
              |||||||:||||||| |||| ||:||||||||| :||:|  :|:||  ||| | |:|||
Db        117 LGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA 176

Qy        280 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
              |||||:|||| | : ||||: |||:||||:||||||||:|||| ||: : |||||:||
Db        177 QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP 236
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Qy        340 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
              |::::| :|||||||  |:   |:|||| ||: | :|| |||:|||||::|||||||||
Db        237 REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT 296

Qy        400 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
                | || :|:|||:|||||||:|||:|| || |:|:||||||||||||||||
Db        297 DSWLQGEIFTCSVVHEALHNHHTQKNLSRSPELELNETCAEAQDGELDGLWTT 349


RESULT 8
GC1M_MOUSE
ID   GC1M_MOUSE     STANDARD;      PRT;   393 AA.
AC   P01869;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-1 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 323-393 FROM N.A.
RX   MEDLINE=82197626; PubMed=6804950;
RA   Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT   "mRNA for surface immunoglobulin gamma chains encodes a highly
RT   conserved transmembrane sequence and a 28-residue intracellular
RT   domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN   [3]
RP   SEQUENCE OF 323-366 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
RN   [4]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01869-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01868-1; Sequence=External;
CC         Note=May be the major isoform;
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   PIR; B02159; G1MSM.
DR   PDB; 15C8; 23-MAR-99.
DR   PDB; 1AE6; 18-MAR-98.
DR   PDB; 1CL7; 12-JAN-00.
DR   PDB; 1F11; 06-FEB-01.
DR   PDB; 1FS8; 29-DEC-99.
DR   PDB; 1KC5; 24-JUL-02.
DR   PDB; 1KCR; 11-MAY-02.
DR   PDB; 25C8; 09-JUL-99.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Transmembrane; 3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .).
FT   DISULFID    244    302
FT   TRANSMEM    340    357       POTENTIAL.
FT   DOMAIN      358    393       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   393 AA;  43386 MW;  4CC88343B7A1CE27 CRC64;

  Query Match             34.5%;  Score 932.5;  DB 1;  Length 393;
  Best Local Similarity   55.0%;  Pred. No. 1.4e-52;
  Matches  177;  Conservative   50;  Mismatches   60;  Indels   35;  Gaps    5;

Qy        133 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQ 190
              :||    ||:      |||                                : | || |    :
Db         56 VLQSDLYTLSSSVTVPSSP------------------------RPSETVTCNVAHPASS 90

Qy        191 KKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 250
              ||: ||    |   :|  |    | ||:    |||:|||||| | |: ||:|||||||
Db         91 TKVDKKIVPRDCGC-KPCIC----TVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVD 142

Qy        251 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 310
              :| :||||:|:|:|| |||| |:|:|||||:|||:| || | ::|||||||||:||:|::
Db        143 ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS 202

Qy        311 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 370
              | |||||||||| ||:|: |||||:|| :::: |::|||||::  |:| || |||: ||
Db        203 AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNG 262

Qy        371 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 430
              ||  ||| | |:::::||:|:|||| | || |: || |:|||:|| ||||:|:|||| ||
Db        263 QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP 322

Qy        431 GLQLDETCAEAQDGELDGLWTT 452
              ||||||||||||||||||||||
Db        323 GLQLDETCAEAQDGELDGLWTT 344


RESULT 9
CD4_MACFA
ID   CD4_MACFA      STANDARD;      PRT;   458 AA.
AC   P79185;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3).
```

```
GN   CD4.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymocytes;
RA   Tatsumi M., Yabe M., Yamada Y.K.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC       receptor interaction. May regulate T-cell activation.
CC   -!- SUBUNIT: Associates with p56-lck (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D63349; BAA09673.1; -.
DR   HSSP; P01730; 1WBR.
DR   GO; GO:0042101; C:T-cell receptor complex; ISS.
DR   GO; GO:0015026; F:coreceptor activity; ISS.
DR   GO; GO:0042289; F:MHC class II protein binding; ISS.
DR   GO; GO:0006955; P:immune response; ISS.
DR   GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR   GO; GO:0030217; P:T-cell differentiation; ISS.
DR   GO; GO:0045058; P:T-cell selection; ISS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Immune response; Repeat; Signal; Lipoprotein; Palmitate.
FT   SIGNAL        1    25       BY SIMILARITY.
FT   CHAIN        26   458       T-CELL SURFACE GLYCOPROTEIN CD4.
FT   DOMAIN       26   396       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    397   418       POTENTIAL.
FT   DOMAIN      419   458       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       26   125       IG-LIKE V-TYPE.
FT   DOMAIN      126   203       IG-LIKE C2-TYPE 1.
FT   DOMAIN      204   317       IG-LIKE C2-TYPE 2.
FT   DOMAIN      318   374       IG-LIKE C2-TYPE 3.
FT   CARBOHYD     42    42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    296   296       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    325   325       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID     41   109       BY SIMILARITY.
FT   DISULFID    155   184       BY SIMILARITY.
FT   DISULFID    328   370       BY SIMILARITY.
FT   LIPID       419   419       S-palmitoyl cysteine (By similarity).
FT   LIPID       422   422       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   458 AA;  50872 MW;  9105479FB5C56FF7 CRC64;

  Query Match             33.9%;  Score 916.5;  DB 1;  Length 458;
  Best Local Similarity   79.6%;  Pred. No. 1.8e-51;
  Matches  183;  Conservative   14;  Mismatches   28;  Indels    5;  Gaps    1;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||:|||||||||||||| ||| ||||||||||||| |||||: ||||||||||
Db          1 MNRGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              |||| |||||||||||:||||||:|||||| | :|||||||||||||||::||||:|
Db         61 ILGIQGSFLTKGPSKLSDRADSRKSLWDQGCFSMIIKNLKIEDSDTYICEVENKKEEVEL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||:|||||||||||||||:|||| ||||||:|||| ||| ||||
Db        121 LVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPGGKNIQGGRTLSVPQLERQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPP 230
              |||||| |:|| |||||||     :  |     |  :  |    | |||
Db        181 TWTCTVSQDQKTVEFKIDIVVLAFQKASS-----TVYKKEGEQVEFSFPP 225


RESULT 10
CD4_MACFU
ID   CD4_MACFU      STANDARD;      PRT;   458 AA.
AC   P79184;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3).
GN   CD4.
OS   Macaca fuscata fuscata (Japanese macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9543;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hashimoto O., Tatsumi M.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC       receptor interaction. May regulate T-cell activation.
CC   -!- SUBUNIT: Associates with p56-lck (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D63348; BAA09672.1; -.
DR   HSSP; P01730; 1WBR.
DR   GO; GO:0042101; C:T-cell receptor complex; ISS.
DR   GO; GO:0015026; F:coreceptor activity; ISS.
DR   GO; GO:0042289; F:MHC class II protein binding; ISS.
DR   GO; GO:0006955; P:immune response; ISS.
DR   GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR   GO; GO:0030217; P:T-cell differentiation; ISS.
DR   GO; GO:0045058; P:T-cell selection; ISS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Immune response; Repeat; Signal; Lipoprotein; Palmitate.
FT   SIGNAL        1    25       BY SIMILARITY.
FT   CHAIN        26   458       T-CELL SURFACE GLYCOPROTEIN CD4.
FT   DOMAIN       26   396       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    397   418       POTENTIAL.
FT   DOMAIN      419   458       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       26   125       IG-LIKE V-TYPE.
FT   DOMAIN      126   203       IG-LIKE C2-TYPE 1.
FT   DOMAIN      204   317       IG-LIKE C2-TYPE 2.
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FT   DOMAIN      318    374       IG-LIKE C2-TYPE 3.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    296    296       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    325    325       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID     41    109       BY SIMILARITY.
FT   DISULFID    155    184       BY SIMILARITY.
FT   DISULFID    328    370       BY SIMILARITY.
FT   LIPID       419    419       S-palmitoyl cysteine (By similarity).
FT   LIPID       422    422       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   458 AA;  50828 MW;  76B3E7EF08185535 CRC64;

  Query Match             33.7%;  Score 910;  DB 1;  Length 458;
  Best Local Similarity   87.5%;  Pred. No. 4.6e-51;
  Matches  175;  Conservative   13;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||:|||||||||||||||| ||| |||||||||||||| |||||: ||||||||||
Db          1 MNRGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||| |||||||||||:||||||:|||||| | :|||||||||||||||||::||||:|
Db         61 ILGIQGSFLTKGPSKLSDRADSRKSLWDQGCFSMIIKNLKIEDSDTYICEVENKKEEVEL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              |||||||||||||:|||||||||||||||||:|||| |||||||:|:|| ||| ||||
Db        121 LVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPGGKNIQGGRTISVPQLERQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV 200
              |||||| |:|| ||||||||
Db        181 TWTCTVSQDQKTVEFKIDIV 200


RESULT 11
GCAM_MOUSE
ID   GCAM_MOUSE     STANDARD;      PRT;   399 AA.
AC   P01865;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma-2A chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Membrane-bound;
CC         IsoId=P01865-1; Sequence=Displayed;
CC       Name=Secreted;
CC         IsoId=P01864-1; Sequence=External;
CC         Note=Probably the major isoform;
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00471; AAB59661.1; ALT_INIT.
DR   PIR; A02154; G2MSAM.
DR   PDB; 1KB5; 08-APR-98.
DR   PDB; 1YEE; 15-OCT-97.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing; 3D-structure; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        6     98       IG-LIKE 1.
FT   DOMAIN      121    220       IG-LIKE 2.
FT   DOMAIN      229    325       IG-LIKE 3.
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   TRANSMEM    346    363       POTENTIAL.
FT   DOMAIN      364    399       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   399 AA;  44020 MW;  4C38138BFAED3FF0 CRC64;

  Query Match             33.5%;  Score 906.5;  DB 1;  Length 399;
  Best Local Similarity   60.5%;  Pred. No. 6.4e-51;
  Matches  173;  Conservative   34;  Mismatches   60;  Indels   19;  Gaps    5;

Qy        179 SGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELLGGPSVF 226
              | ||     || |    :  ||: ||:     | |||   |  |      | ||||||||
Db         72 SSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---PCKC----PAPNLLGGPSVF 124

Qy        227 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 286
              :|||| || |||| :| |||||||||| :||:|: :|:|: |||| |:|:   | |||| |
Db        125 IFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLR 184

Qy        287 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
              ||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||  :|:||
Db        185 VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKK 244

Qy        347 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 406
              ||:|||:|  | | || ||| :||: | ||| | |||||||:|:|||| |:|  | : |
Db        245 QVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERN 304

Qy        407 VFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
               :||||:|| ||||:| || | :||| ||: ||||||||||||||
Db        305 SYSCSVVHEGLHNHHTTKSFSRTPGLDLDDVCAEAQDGELDGLWTT 350


RESULT 12
CD4_MACMU
ID   CD4_MACMU      STANDARD;      PRT;   458 AA.
AC   P16003; Q29617;
DT   01-APR-1990 (Rel. 14, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3).
GN   CD4.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90182664; PubMed=2107024;
RA   Camerini D., Seed B.;
RT   "A CD4 domain important for HIV-mediated syncytium formation lies
RT   outside the virus binding site.";
RL   Cell 60:747-754(1990).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymocytes;
RA   Hashimoto O., Tatsumi M.;
RT   "Molecular cloning and expression of macaque CD4s.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 28-424 FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=93049640; PubMed=1425921;
RA   Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT   "Cloning and sequences of primate CD4 molecules: diversity of the
RT   cellular receptor for simian immunodeficiency virus/human
RT   immunodeficiency virus.";
RL   Eur. J. Immunol. 22:2973-2981(1992).
RN   [4]
RP   SEQUENCE OF 107-192 FROM N.A.
RX   MEDLINE=98320644; PubMed=9656488;
RA   Harris E.E., Disotell T.R.;
RT   "Nuclear gene trees and the phylogenetic relationships of the
RT   mangabeys (Primates: Papionini).";
RL   Mol. Biol. Evol. 15:892-900(1998).
CC   -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC       receptor interaction. May regulate T-cell activation.
CC   -!- SUBUNIT: Associates with p56-lck (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M31134; AAA36838.1; -.
DR   EMBL; D63347; BAA09671.1; -.
DR   EMBL; X73326; CAA51752.1; -.
DR   EMBL; AF057385; AAC25129.1; -.
DR   HSSP; P01730; 1WBR.
DR   GO; GO:0042101; C:T-cell receptor complex; ISS.
DR   GO; GO:0015026; F:coreceptor activity; ISS.
DR   GO; GO:0042289; F:MHC class II protein binding; ISS.
DR   GO; GO:0006955; P:immune response; ISS.
DR   GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR   GO; GO:0030217; P:T-cell differentiation; ISS.
DR   GO; GO:0045058; P:T-cell selection; ISS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Immune response; Repeat; Signal; Lipoprotein; Palmitate.
FT   SIGNAL       1     25
FT   CHAIN       26    458       T-CELL SURFACE GLYCOPROTEIN CD4.
FT   DOMAIN      26    396       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   397    418       POTENTIAL.
FT   DOMAIN     419    458       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      26    125       IG-LIKE V-TYPE.
FT   DOMAIN     126    203       IG-LIKE C2-TYPE 1.
FT   DOMAIN     204    317       IG-LIKE C2-TYPE 2.
FT   DOMAIN     318    374       IG-LIKE C2-TYPE 3.
FT   CARBOHYD   296    296       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD   325    325       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID    41    109       BY SIMILARITY.
FT   DISULFID   155    184       BY SIMILARITY.
FT   DISULFID   328    370       BY SIMILARITY.
FT   LIPID      419    419       S-palmitoyl cysteine (By similarity).
FT   LIPID      422    422       S-palmitoyl cysteine (By similarity).
FT   CONFLICT    42     42       N -> T (IN REF. 1).
FT   CONFLICT    62     62       L -> S (IN REF. 3).
FT   CONFLICT    67     67       L -> S (IN REF. 2).
FT   CONFLICT   169    169       I -> L (IN REF. 2).
FT   CONFLICT   191    191       K -> N (IN REF. 3).
FT   CONFLICT   248    248       S -> P (IN REF. 2).
FT   CONFLICT   265    265       R -> Q (IN REF. 3).
FT   CONFLICT   349    349       A -> T (IN REF. 2).
SQ   SEQUENCE   458 AA;  50884 MW;  8BB80339FAFEC808 CRC64;

  Query Match             33.5%;  Score 904;  DB 1;  Length 458;
  Best Local Similarity   87.0%;  Pred. No. 1.1e-50;
  Matches  174;  Conservative   13;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
              ||||:||||||||||||||| ||| |||||||||||||| |||||: ||||||||||
Db          1 MNRGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK 60

Qy         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
              ||| || |||||||||:||||||:|||||| | :|||||||||||||||||::||||:|
Db         61 ILGIQGLFLTKGPSKLSDRADSRKSLWDQGCFSMIIKNLKIEDSDTYICEVENKKEEVEL 120

Qy        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
              ||||||||||||||:|||||||||||||||||:|||| |||||||:|:|| ||| ||||
Db        121 LVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPGGKNIQGGRTISVPQLERQDSG 180

Qy        181 TWTCTVLQNQKKVEFKIDIV 200
              |||||| |:|| ||||||||
Db        181 TWTCTVSQDQKTVEFKIDIV 200


RESULT 13
CD4_MACNE
ID   CD4_MACNE      STANDARD;      PRT;   458 AA.
AC   Q08340; P79196;
DT   01-FEB-1995 (Rel. 31, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3).
GN   CD4.
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hashimoto O., Tatsumi M.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 28-424 FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=93049640; PubMed=1425921;
RA   Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT   "Cloning and sequences of primate CD4 molecules: diversity of the
RT   cellular receptor for simian immunodeficiency virus/human
RT   immunodeficiency virus.";
RL   Eur. J. Immunol. 22:2973-2981(1992).
CC   -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC       receptor interaction. May regulate T-cell activation.
CC   -!- SUBUNIT: Associates with p56-lck (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
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